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Title:
Perfect score:
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-QB=1gsued Patents NA -QFMT=fastap -SUFFTX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS-Dits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-NO XLPXY -NO MMĀP -LĀRĢĒGŪERŸ -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=7 -XGAPEXT=7  
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model -DEV=xlh
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                             Result
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                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
165
165
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Ygapop 10.0 , Ygapext
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Copyright (c) 1993 - 2002
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                                                         US-09-276-531-47
US-08-924-345-1
US-08-814-095-7
US-08-804-227C-1
US-09-295-593-37
US-09-295-568A-11
US-09-154-750A-75
US-08-320-559-1
US-08-320-559-1
                  US-08-327-392-1
US-08-306-691B-55
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Compugen Ltd
                                  Sequence 1, Appli
Sequence 37, Appl
Sequence 11, Appl
Sequence 75, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 7, Appli
Sequence 1, Appli
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ALIGNMENTS

US-09-276-531-47

Sequence 47, Application US/09276531 Patent No. 6183968

GENERAL INFORMATION: APPLICANT: Bandma: COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORE Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION APPLICANT: CORRESPONDENCE ADDRESS: APPLICANT: ATTORNEY/AGENT INFORMATION: NUMBER OF SEQUENCES: APPLICANT: STREET: 3174 POR CITY: PALO ALTO APPLICATION NUMBER: COUNTRY: ADDRESSEE: 94304 CALIFORNIA 3174 PORTER DRIVE USA Hillman, Jennifer L. Yue, Henry Lal, Preeti Bandman, Olga INCYTE PHARMACEUTICALS, INC Floppy disk March 27, 1998 Roopa 60/079,677

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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   803 SerThrValAsnAspLysLeuGluLeuGlnGluCysLeuGluHisGlyArgljeAlaLys 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     783 AlaAlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProLeuAla 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 GCTGCTCACAGGGCCCGATACTTCTGGGGCAACCTACCCGGGATGAACAGGCCCGTGATA 296
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                  Length:
Matches:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INPORMATION:
TELEFHONE: (650) 845-0555
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 207) base pairs
TYRE: nucleic acid
STRANDENESS: single
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748.00
81.95%
73.66%
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| IMMEDIATE SOURCE:
| LIBRARY: TESTTUTO2
| CLONE: 1271435
| US-09-276-531-47
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Best Local Similarity:
Query Match:
DB:
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Sequence 1. Application US/0892495

GENERAL INCOMATION:
PAPLICANT: LEGASTRELOS IS Eabelle Christine, Marie-Andree Christine, Marie-Andree Christine, Marie-Christine, Marie-Christine Christine, Marie-Christine Christine Christine, Marie-Christine Christine Christine Christine, Marie-Christine Christine Christine
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rpGlyLysLeuArg 297 	heGlyIleGlyGluLeuValTx 	278 ProGluTyrGluAspGlyArgGlyI	рь 11
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/sValGlyArg 47 :: 3CGGCCGC 995	ArgGlnGluProSerAlaThrAlaArgLysV ::::: cccgccagccccrcccgrgccTTTagcgc-	35Ar 	Dy Cy
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GluGlyGluGlu 25 GAGGGTCGACGA 878	erSerSerLeuGluArgGluAspAspArgLySG] 	6 ProGlyAspThrSerSerSerSe ::: 822 CCCGGCCCCACCGCGAGCAGCGA	Qy 8
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	Mismatches: 212 Indels: 151 Gaps: 24	ocal Similarity: 22.04% Match: 3.36% 4	Best Lo Query M DB:

	LASSII ORNEY, AME: EGISTI EFEREI	** ** ** ** ** **
	APPLICATION NUMBER: US/08/814,095 FILING DATE:	
	TING SYSTEM: ARE: Patentl	
	PUTER READABLE FORM: EDIUM TYPE: Floppy disk	
	COUNTRY: U.S. ZIP: 48334	·· ·· ·
	armington Hills	
	ESSEE: KOHN & ASSOCIATES	•
	R OF SEQUENCES: 7	
	NVENTION:	
	AFFLICANT: Soled, neimona APPLICANT: Zakut, haim APPLICANT: Shani Moshe	
	PPITCACIO 25183 RMATION:	
	SULT 3 -08-814-095-7/c	US
38	2190 CGGGCCCACCCCGGCCGCCGCCCCACCGCACGACGACACGCGCGCCC 22	ф
ř	442 aAlaTyrAlaProProProProAlaLysLysProArgLysSerThrThrGluLysPro 46	γQ
2189	2169 CGAGGAGAGGGAACCAGCGAC	뫄
442	422 uGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGluAlaAl	9
2168	2127 GCTGCAGGTCGCGACGCCGGCGCGCGCGCAGGGCGCCGCGCGGGA	ф
422	402 tlleGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGl	δδ
2126	2070 CCTGTACGACCGGCTCATCGGCGACGCCGGCGACGGAGACGCAGTTGGCGCTGAC	ם
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2069	2010 TCGCAACGCGACCGGGGTGCTGATCGCGGCCGCAGCCGAGGAGACGACGGCGCGTGTACTT	Dp.
388	372 aSerSerArgAlaGlyLysLeuPheProAlaCysHisAspSerAspGlu	Ş
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1949	1890 GGCCTGCCGAACCGCCGCGTGGCCCCGCTGGCCATCGCGGAGCTCGCCGAGCGGCC	뫄
352	334 lValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPheHisGl	γQ
1889	1830 CGTGCCGGAGCCCGTCTGCCTCGACGACCGCGAGTGCTTCACCGACGTGGCCCTGGACGC	đg
334	327PheGlyAspGlyLysPheSerVa	δ
1829	1770 GCGCCCGGACGTGCGCCGCTTCGCGGCTGGAGCGTCCTCGCGGGCCTGCTCGCCGCC	뫄
326	318 AlaGluGly-ThrArgTrpValMetTrp	γQ
1769	1743 GCC	ఠ
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NAME/KEY:
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INFORMATION FOR SEQ ID NO: 7:
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LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANBEDRESS: double
TOPOLOGY: linear nucleic acid
MOLECULE TYPE: other nucleic acid
DESCRIPTION: promotor, ACHE gene and ARS gene"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOUNCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
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OTHER INFORMATION: /number= 16
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                                                23826 CAGGGGTCCACTGCCCTCACCTCTTCCCGGGAACTGGGGCCGAGGTCCAGGTGAG 23767
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                                                                                                                                           237 GluAlaSerProProAlaValGln---GlnProThrAsp-------Pro 249
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                  269
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                                                                                                                                                                                                                                      ArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLysAlaLysVal 216
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                                                                                                                                                                                                                                                                                                                                                                                                    Gly-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACCCAGGAGCCAGAGGAGGAGGAGAAGGAGTGGGGAAGCCAGGGAAGGCGTGTGCAGC 24130
nAlaThrLysAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGl 289
                                                                                                             AGGCAGACACCCATATCCAGACAAATGCAGGGAACAGAGAGGAGGAGCACCCTTTCTGCTCCG
                                                                                                                                                                                                         IleAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSerGlnLysValGlu
                                                                             AlaSerProThrValAlaThrThr-ProGluProValGlyGlyAspAlaGlyAspLysAs
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/number= 15
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                                                                                                                                                                          ----ACACAGGCCAGCGGGCAGGAGGGGGAAAGAGATC 23887
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Matches:
Conservative:
Mismatches:
Indels:
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ا تنا	GGATCAAAATTCCCCGGGTGGGAAC	23182	B &
623		ט ע	Ş
608 23183	GGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsn	594 23242	P &
23243	CGAGCCG	23266	DЬ
594	spProTrpAsnCys	574	γQ
23267		0	В
574	uCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGl		Ş Ş
23308	BGCGCTCCCCGCCCGAGCCAGGAGCCGGGAACTTGGGGAGG	23349	ДD
557	sGlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGl	537	γQ
23350		23350	ДЬ
537	${\tt eLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrIleCysCy}$	517	γQ
23350		23350	Дb
517	nValThr LeuGlu His ProLeuPheIleGlyGlyMetCysGln AsnCysLysAsnCysPh	497	γQ
23350		23350	ф
497	${\tt rGluValArgGlnLysCysArgAsnIleGluAspIleCysIleSerCysGlySerLeuAs}$	477	Q
23350		23373	D
477	rThrGluLysProLysValLysGluIleIleAspGluArgThrArgGluArgLeuValTy	457	Ş
23374	TGCACGCCGCCGCCGAG	23394	Db
457	lGluProGluAlaAlaAlaTyrAlaProProProProAlaLysLysProArgLysSerTh	437	γQ
23395	TCGAGAGCCCCCATCCGTCTGAAGCTGCCG	23425	ДD
437)ProGluGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpVa	417	Ş
23426		23448	дъ
417	lGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGl	397	ρ
23449	CGGGTTCCCATCAGCTGCGCACGC-TCCCAGCGCAGCCCCAGCAAACAGGCT	23499	문
397	>AlaCysHisAspSerAspGluSerAspSerGlyLysAlaValGluVa	378	Ş
23500	eccce	23522	Db
378		358	Ş
23523	CCCAACCCTGCCCCTTCTCATCCAATGT	23550	ф
358	uLysLeuMetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGl	338	Ş
23551	TTCAGGGTGTGGAAGCCTCAGGTCCCGGGGTCCCCCAAATCCTGCCTAGTCCACTCCCCA	23610	Дb
338	161	326	Ş
23611	GCTCTCCTGGGTCGGCCAGACCCGGGGCCCTGGGGGGGGGG	23661	DЪ
326	hrGlyArgSerArqAlaAlaGluGlyThrArgTrpValMetTr	306	Ş
23662	CC	23706	뫄
306	TrpTrpProGlyArgIl	289	Ş
23707	GGCACCAGAAGCCTCAGTCCACGAACAGGCCACCCGACAGGGGGGGG	23766	문

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623 oAla.....GluLysArgLysProlleArgValLeuSerLeuPheAspGl 638
                                                                                                                                                                 Sequence 1, Application US/08804227C
Parcent No. 5876991
Parcent No. 5876991
Parcent No. 5876991
Parcent No. 5876991
Papticant: Marcoss, Stuart A.
PAPLICANT: Rulescoss, Stuart A.
PAPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                         Db 23082 ------GGGGTGGTGCTGCTGGAGATT 23059
                                                                638 yıleAlaThrGlyLeuLeuValLeuLysAspLeu 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: FORDY disk
COMPUTER: IBM COMPALISH
COMPUTER: ASCIIOOS) Text only
CURRENT APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
ATTORNEY AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTATION NUMBER: X.8231
TELECHONE: 317.76-2459
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
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TYPE: nucleic acid
STRANDEDNESS: single
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14351..19945
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20010..31199
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33.46%
24.08%
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36249..41774
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31232..36067
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION: 816..14234
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Query Match:
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US-08-804-227C-1
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23905 CCGTCCTCGAGCAGGGGTCCGGCTCGAGCAGCCGAGTCCAGACGTC-GACCAGACC 23847
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                                                                                                                                                                                                                               23786 CGGGACGGCCGGGGCCCCACGACCACGACCACGACGCCTCTTCGGCGACGACGTCCG 23727
                                                                                                                                                                                                                                                                                                                       23726 CAGGGGGGGGGGATCGGCCGGATCACAGGCGCCACGGTCACCCGTGCCGCCACACGGC 23667
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                                                                                                                                                                                                  21 LyselugiygluglugluglugluasnArgGlyLys------GjugluArgGln 36
                                                                                                                                                                                                                                                                                   37 GluProSerAlaThrAlaArgLy8ValGlyArgProGlyArgLy8ArgLy8Hig-ProPr 56
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                                        Percent Similarity:
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                                                                    Pred. No.:
                                                                                                                                                                 SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             equence 37, Application US/09295593 atent No. 6417169
                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/295,593
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Alping H.
APPLICANT: LEE, Yoon S.
APPLICANT: LEE, Yoon S.
TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL
TITLE OF INVENTION: GROWTH
FILE REFERENCE: 032396-046
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                                                                                                                          LENGTH: 4350
TYPE: DNA
ORGANISM: Human
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                             Local Similarity:
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Matches:
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                                                                                                                GlnProThrAspProAlaSerProThrValAlaThrThrProGluPro-----Val
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AspGlyArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrp ||||||:::
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OF INVENTION: Compositions and Methods commended	VENUTION: Infections HEQUENCES: 15 MCE ADDRESS: Modcock, Washburn, One Liberty Place, 46th	COUNTRY: USA ZIP: 19103 COMBUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBR: US/08/458,568A FILING DATE: US-03/UNE-1995 DDIOD ADDITORNOW: 435		REFERENCE/DOCKET NUMBER: DFCI-0029 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100 TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 11.	JENGTH: 1201 base pairs TYPE: nucleic acid TRANDEDNESS: double TOPOLOGY: linea	NO:	Scores: 0.00942 Length: 161.00 Matches: 28 938	arity: 20.89% Conse	SerGlybroglyAspThrSerSerSerSerLeugluAspAspArgLys CCGGGGCCCGGT	5937	ProProvalgluserserasp ::: CCTCCTCTACCATGG	6048 AGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	TOTAL CONTROL OF THE STREET OF
_		Oy 338 GluLysLeuMetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyzAsnLys 357 Db 2546 GCCAAACTCCTCACTCTGGCTGGGCCAACACA	T 247	Oy 398 GlnAsnLysGlnMetlleGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLys 416		Oy 452 LysProArgLysSerThrThrGluLysProLysValLysGlullelleAspGluArgThr 471 Db 2270 GGGCCGAGGGCATGGAATGGGAACAGGAGGGGGGCTCAGACCATG:	Db 2216 TTGGAGAATCTTAGCGGACTTTGGCCTGATCCATACAGATATCGTAGTTGCTTAGA 485 OY 485 nlleGluAspileCyslleSerCysGlySerLeuAsnValThrLeuGluHisProLe 504 Db 2159 TATCCTTAGATATCTTTGCTTTTGGCTTTGGCTTAGA		TTC	1979 TGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	1919	Db	; Parent No. : \$82139 ; GENERAL INPORMATION: ; APPLICANT: Schaffer, Priscilla A. ; APPLICANT: Yeh, Lily	

6965	6936 GCGGGGCCCGGGCCCGACTTCCC	밁
(L)	ProAlaCysHisAspSerAspGluSerAspSerGlyLys 	Ş
6935	6918 ACGAGGAACGGGCAGGGG	ᅡ
373	nLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGlnValAlaSer 	Ş
6917	6882CCGATCCGGCGGTTTCCGCTTCCGCATGCTA (용
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333	314 ArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLysPheSer :	Ş
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313	294 GlyLysLeuArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMetThrGly 3	8
6821	6807 CCGCGCCATCTGCCA 6	р
293	lyArgGlyPheGlyIleGlyGluLeuValTrp	8
5806	6759 GGGGGCCCGTGGCCGGCCCGTTGGTCGAACCCCCGGCCCGCCC	망
273	ThrLysAla 2	
5758	6699 GGCGGGCCCACCCGAACGGAATTCCATTATGCACGACGCCCCGCCCCGACGCCGGCACGCC 6	F
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647	6621 GGGCGTCCTCGGGCTCATATAGTCCCA 6	뭥
29	AlaValMetAsnAlaValGluGluAsnGlnAlaSer 2	γQ
620	6561 TGGCGGTCCGCGTCGGGTCGTGGATCCGTGTCGGCAGCCGCGCTCCGTGTGGACGATCG 6	ర్జ
09	LysArgGlu 2	Ş
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461	6402 GCGAGACCCACGGACCCCGACGACCCCGCCGTCGACGCGGAACTAGCGCGGACCGGTCG 6	B
68	MetLysMetGluGlySerArgGlyArgLeuArgGly 1	
401	CGGCGGACGTAGCACGGTAGGTCACCTACGGACTCTCGATGGGGGGAGGGG 6	7
148	ThrLysGluGlyArgGlyAlaSerAlaGlyGluGlyLysGlu	ર્
341	6282 AGCCGGGGCGCTGCTTGTTCTCCGACGCCATCGCCGATGCGGGGGGGG	뫄
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281	6222 CCCCCCCCTCGTCGCGGTCTGGGCTCGGGGTGGGGGCCCGTCGGTGGGGCCCGGGG 62	뮹
.12	02 SerProAlaAlaGlyGlnLysGlyGlyAlaPro 1	8
221	6162 GGTCGGGGTCGTGGTCGGGGTCGTCCCGCCCTCCTCCGTCTCCGGCGCCCCACCCGAGGG 62	당
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SEQUENCE 75, Application US/09154750A
PATENT NO. 6432640
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: 593-Induced Apoptosis
FILE REFERENCE: 1107.75357
CURRENT FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US/09/154,750A
CURRENT FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/059,153
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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US-09-154-750A-75
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DB:
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Pred. No.:
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; ORGANISM: Homo
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Best Local Similarity:
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LENGTH: 2608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GÁCGCCGGGACCAACGGGACGGCGGCGGCCCAAGGGCCGCCTTGCCGCCCCCCA 7091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGGCCGGCGGGGACCGCCCAAGGGGGGCGGGCCGCCGGGTAAAAGAAGTGAGAAC 7151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sLysProArgLysSerThrThrGluLysProLysValLysGluIleIleAspGluArgTh 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspMetTrpValGluProGluAla-AlaAlaTyrAlaProPro-----ProProAlaLy 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rArg-----
                                                                                                                             GTCGGAGAAGCAGGACGTGCAGGAGCAGCTGGACCTGCAACACAAAAAATGCCAGGAAGC 790
                                                                                                                                                          SerAlaThrAlaArgLysValGlyArgProGlyArgLysArgLysHisProProValGlu 58
                                                                                                                                                                                              GAGGATCTCGGAACTGCAGTGGAGCGTGATGGACCAGGAGATGCGGGTGAAGCGCCTGGA 730
                                                                                                                                                                                                                                GluGlu-----
                                                                                                                                                                                                                                                                TCTGGCCCAGGC-----
                                                                                           SerSerAspThrProLysAspProAla---ValThrThrLysSerGlnProMetAlaGln 77
                       Asp-----SerGlyProSerAspLeuLeuProAsnGlyAspLeuGluLysArgSerGlu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
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159.50
32.04%
21.13%
3.25%
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                                                                                                                                                                                                                             ---GlnGluGluAsnArgGļŅLysGluGluArgGlnGluPro 38
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-061-376-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSECHII RC-DOS/MS-DOS
SOFTWARE: PSECHII RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,376
FILING DATE: 13-MAY-193
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9387
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)546-4737
TELECHONE: (619)546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: (619)346-9392

**MPORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 11907 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: unk
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                       2767
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2707 GCTTTGTATCCTGTGGGTAGGGTTTCCAAAGAGAAGGTTGTTGGTGAAGATGTTGCCACT 2766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2880 TATAAAGAAAGGGAGAGGAAATCTGGAAAAAACCAACTTGGACCTCGGCCCAACTGCCCC 2939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2647 AATAAGCGGGAGTCAAGGAAAAGAGAAAAAGGGAAAAAGGGATCAGAAATTCAGAGTAGTTCT 2706
3060 GAGGGTTGCCAGCCTCCTAAAAAAAGGCCCAAAGCTCAGCTCTGCAAGATTGAGAAGAGTAA 3119
                                                                           2940 ATCCCTGGAGAAGGAGAAAACCCTCTGCCTTTCCACTCCTTCATCTAGCACTGTTAAACA 2999
                                                                                                                                                                                           113 AlaGluGlyGluGlyThrGluThrProPro-----
                                 130 AsnGlyCysCysValThrLysGluGlyArgGlyAla------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 ThrAlaArgLysValGlyArgProGlyArgLysArg---LysHisProProValGluSer 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 SerSerSerLeuGluArgGluAspAspArgLysGluGlyGluGluGluGluGluAsn
                                                                                                                                                                                                                                                                 93 ArgSerGluProGlnProGluGluGlySerProAlaAlaGlyGlnLysGlyGlyAlaPro 112
                                                                                                                                                                                                                                                                                                                                                                                                                 60 SerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGlnAspSer 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 GlyPro-----SerAspLeuLeuProAsnGlyAspLeuGluLys 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                         GGGACTGATATTACTTCTGTGACTCTTGGGGATACAACAGCTGT-CAAAACCAAAATACT 2879
                                                                                                                                                                                                                                                                                                                                                                                     TCATCTTCTGCCAAA-----AAAGCAACAGGGCGGAAGAAGTCTTCATCACATGATTCT 2820
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158.50
32.17%
19.12%
3.23%
                                                                                                               -----GluAlaSerArgAlaValGlu 129
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Matches:
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Indels:
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148
101
275
254
                                       .---- 141
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459	l slysProArgLysSerThrThrGl	451	Ş
4007	TCCCAAAACCACTCCTAGTGAGCCCAAGAAAAAGCAGCCTCCACCACCAGAATC	3954	40
451	TyrThrAspMetTrpValGluPro	431	Q
3953	CCAGCCAGCACTGGTCATCCCGCCCTCAGCCACCTACTACAGGACCGCCAAGAAAAGAAGT	3894	B 6
ءة د	TGGGCCTGAATCCAAACAGGCCACCACTCCAGCTTCCAGGAAGTCAAGCAAG	3834	} B
\vdash	rGlyProLysGlyLeuGlu	413	Ş
3833	CGTCGAGGAAAAGAGT	3792	Дb
413	sAlaValGluValGlnAsnLys	393	Qy
3791	CCATCAGCAAGAGGATCCTGCCCCAAAG-AAAAGCAGTAGTGAGCCTCC	3733	뫄
393	/GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGlyLy	377	8
3732	: ::	3673	Дb
376	5	370	δ
3672	TGCAGAAGCAAGCTGTGAAAA-AGAAAGAGAAAAAGTCTAAGACCAGTGAAAAG	3614	망
370	eHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeu	350	δ
3613	AGCAGTGCTGCAAGATGAGAAAATGTCAGAATCTACAATGGATGCCTTCCAAAGCCTACC	3554	B
350	eSerValValCysValGluLysLeu	332	Ş
3553		3509	멍
332	rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTr	312	Ş
3508	GTGGGCAGTGTCCCGGC	3461	뭥
312		292	Qγ
3460	CAAGGCACCCCAGGAACCTCCAGTAAAGAAAGGACC	3411	멍
292		272	δδ
3410	TGTCACTAGAAA	3399	뭥
272	oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy	252	ð
3398	:GAAGATGCTGAACCTCTTGCTCCACCCATCAAACCAATTAAACC	3355	Д
252	rGlnLysValGluGluAlaSerProProAlaValGln	232	S
3354	ACGAGAAAAGATTTTGTCTTCCATGGGGAATGATGACAAGTCATCAATTGCTGGCTCA	3297	망
232	sLysAlaLysValI	212	ð
3296		3280	망
212	rTyrIleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAla	192	Ş
3279	_	3240	뫄
192		172	δ
3239	o-	3180	망
172		152	Ş
3179		3120	DD DD
152	SerAlaGly	142	á

us-09-720-086-5.rni

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	LysProlysVallysGlu	IleIleAspGluArgThrArg	GlubrgleuvalTyrGluvalArgGlnLysCysArgAsnIleGlubsp 488 :::	GEGERGEGENTERGERUTTERGERTEGENTGENTERGERTEGENTGENTERGERTEGENTGENTEGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTURGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTERGENTGENTGENTGENTGENTGENTGENTGENTGENTGENT	Y 513 G 434		CysThr11eCys	-GlyargGluValLeuMetCysGlyasnasnasnCysCysArgCysPheCysValGluCy 558	euvalGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTr 577 ::: :CTGGGACCAAACTACCCCACCAAAGAAGAAGAAGAAGAAGTCTG 4571	DABNCYSTYZMEtCYSGIYHisLySGIYTHZTYZGIYLEULEUAZGAZGAZGGIUASPTz 597	DProSerargLeuGlnMetPheAlaAsnAsap 610 .:::::	US/08320559	r.o	, Eli Diagnostics, Therapeutics and Methods for	Detection and Treatment of Acute Leukemias Resulting from Chromosome Abnormalities in the	44. region 4.4.	K Washburn Kurtz Mackiewicz & No. 5633135ris			FORM: SKETTE: 3.5 INCH. 1.44 Mb STORAGE		RFECT 5.1 DATA:	/320,559
	3 ·· 4					ω—⊢			sValAspLeuL 	pAsnC GATCT		-559-1 e 1, Applic	5633 FORM T:	APPLICANT: Canaani TITLE OF INVENTION:	E OF INVENTION: E OF INVENTION:	NUMBER OF SEQUENCES:	DRESSEE: W	CITY: Philad STATE: PA		READ	COMPUTER: IB	FTWARE: WC	APPLICATION N
Db 4008	Oy 459 Db 4068	Oy 466 Db 4128	Oy 473 Db 4188	Oy 489	, 4	Oy 513 Db 4350	Qy 528 Db 4410	Qy 539 Db 4470	Oy 558 Db 4524	Oy 577 Db 4572	Oy 597 Db 4632	RESULT 9 US-08-320-	; Patent No.; GENERAL IN	APPLI	TITE	NUMBER	ADE	CIT	COL	, COMPUTER	(C)	SOF	APE

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2404 GCTGACAAGAGGTGGAGAAAGACAAAAGGAGAAAAAGGAG 2463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2697 TATAAAGAAAGGAAGAAAAATCTGGAAAAAACCAACTTGGACCTCGGCCCAACTGCCCC 2756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2464 AATAAGCGGGAGTCAAGGAAAAGGAAAAAGGGATCAGAAATTCAGAGTAGTTCT 2523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2584 TCATCTTCTGCCAAA-----AAAGCAACAGGGCGGAAGAAGTCTTCATCACATGATTCT 2637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 AsnGlyCysCysValThrLysGluGlyArgGlyAla------------ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 ThrAlaArgLysValGlyArgProGlyArgLyBArg---Ly8HisProProValGluSer 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 SerAspThrProLysAspProAlaValThrLysSerGlnProMetAlaGlnAspSer 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SerSerSerSerLeuGluArgGluAspArgLysGluGlyGluGluGluBnn 29
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Matches:
Conservative:
Mismatches:
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FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

FADLICATION DATA:

FILING DATE: 14 MAY 1993

FRICA PAPLICATION DATA:

APPLICATION NUMBER: US/07/971,094

FILING DATE: 30-0CT-92

REING APPLICATION NUMBER: US/07/971,094

FILING DATE: 11-0CT-92

RPLICATION NUMBER: US/07/808,830

FILING DATE: 11-0EC-91

APPLICATION NUMBER: US/07/805,093

FILING DATE: 11-0EC-91

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 33,229

ATTORNEY/AGENT INFORMATION:

TELECHONE: (215) 568-319

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 14255

TYPE: nucleic acid

STRANDEDIESS: single

'ANTI-SENSE: No

US-08-320-559-1
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158.50
32.17*
19.12*
3.23*
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set Local Similarity:
tery Match:
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ed. No.:
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31 TyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProProAlaLy 451	4.	8
	ω 7	밁
0ProProGluGluGluLysAsnProTyrLysGluVa		S i
13 rGlyProLysGlyLeuGlu 419 ::	413 3651	음성
3 sAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSe 413	393 3609	음 성
7GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGlyLy 393	37 355	유
O nValAlaSerSerArgAla	370 3490	음 성
0 eHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGl 370	350 3431	음 성
2 eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPh 350	332 3371	\$
2 rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLysPh 33	332	유 상
2 lTrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMetTh 31	327	유
2 sAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuVa 292 	27: 322!	유 왕
2 oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLy8AsnAlaThrLy 27 6 TGTCACTAGAAA 32	25; 321:	유 성
2 rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr 25	23; 317;	ያ የ
2 SLYSAlaLYSVallleAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSe 23 ::::	212 3114	유 성
2 rTyrIleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLy 212	309	ફ
2 pGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTy 192 ::: :::::: 7 AAAACGAGCTGTGTTTCCTGATGACATGCCCACCCTGAGT	172 3057	음 성
rAsnIleGluSerMetLysMetGluGlyS 	152 2997	유
2	142 2937	β δ
	2877	Вb

	PERATING SYSTEM: PC-DOS SOFTWARE: WORDPERFECT 5.1	ဖ ဝ	
	IBM		
	READABLE FORM:		
	, IZ ::	. O (
	One Liberty Place - 46th niladelphia		
	EE: Woodcock Washburn Kurtz	, e	
	R OF SEQUENCES:	NUMBER	
	OF INVENTION: Antibodies for Leukemi OF INVENTION: Treatment	TITLE	
	CANT: Canaani, Eli OF INVENTION: ALL-1 Polynucleotides and Monoclon	TITLE	
	INFORMATION: CANT: Croce, C	GENERAL APPLI	
	se 1, Application US/08327392	Sequenc	
	-392-1	RESULT 1 US-08-32	C #1
	9 GGATGCACAGTGGTCTCATGATTTCTCACTGTGTCATGAT 4488	Db 444	п
	7 pProSerArgLeuGlnMetPhePheAlaAsnAsnHisAsp 610	0у 59	_
4448	GCTGTGGATCCACAACTCCAGGCA	Db 438	н
597	7 pAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgArgGluAspTr	Оу 57	
4388	CCTGGGACCAAACTACCCCACCAAACCCACAAAGAAGA	Db 4341	п
577	. ໝັ	Ωу 55	_
4340	7 TACAAAGCAGCTGCTGGAGTGTAATAAGTGCCGAAACAGCTATCACCCTGAGTG	Db 428	н
558	uVa	Qy 53	0
4286	7 GGAAAATTGGTGTTGTCGTCGTTGCAAATTCTGTCACGTTTGTGGAAGGCAACATCAGGC	Db 422	н
538	YTyrGlnSerTyrCysThrIleCysCysGly	Oy 528	0
4226	TIGTGAGCCCTTCCACAAGTTTTGTTTAGAGGAGCACGAGCGCCCTCTGGAGGACCAGCT	Db 4167	ы
528	sLysAsnCysPheLeuGluCysAlaTyrGlnTyrAs	Qy 513	Ω
4166		Db 4125	
513	sGlySerLeuAsnValThrLeuGluHisProLeuPheIleGlyGlyMetCysGlnAsnCy	Оу 493	Ω
4124	::: - GGGAGGCTTAGGAATCTTGACTTCTGTTCCTATAACACCCAGGGTGGTTTGCTTTCTCTCT	Db 4065	6
493		Оу 489	O
4064	AGTCCACAGGATCAGAGTGGACTTTAAGGAGGATTGTGAAGCAGAAAATGTGTGGGAGAT	Db 4005	U
488	euValTyrGluValArgGlnLysCysArgAsnI	у 473	δ
4004	GAACAT	b 3945	뫄
472		у 466	Š
3944	8=	b 3885	망
465	uLysProLysValLysGlu	у 459	δ.
3884		b 3825	밁
459	sLysProArgLysSerThrThrGl	у 451	δō
3824	TCCCAAAACCACTCCTAGTGAGCCCAAGAAAAAGCAGCCTCCACCAGAATC	b 3771	ᄱ

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2464 ANTAAGCGGGAGTCAAGGAAAGAAAAGGAAAAAGGATCAGAAATTCAGAGTAGTTCT 2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2524 GCTTTGTATCCTGTGGGTAGGGTTTCCAAAGAGAAGGTTGTTGGTGAAGATGTTGCCACT 2583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2584 TCATCTTCTGCCAAA-----AAAGGAAGAGGGGGGAAAAAGTCTTCATCATCATGATTCT 2637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 ArgSerGluProGlnProGluGluGlySerProAlaAlaGlyGlnLysGlyGlyAlaPro 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 -----GlualaSerArgAlaValGlu 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ThralaArgLysValGlyArgProGlyArgLysArg---LysHisProProValGluSer 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 SerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGlnAspSer 79
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NDATA:
APPLICATION NUMBER: 07/971,094
FILING DATE: 30.0CT-92
PRIOR APPLICATION NUMBER: 07/871,094
FILING DATE: 30.0CT-92
PRIOR APPLICATION NUMBER: 07/805,093
FILING DATE: 11-8CC-91
APPLICATION NUMBER: 07/805,093
FILING DATE: 11-8CC-91
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,229
FILING DATE: 11-8CC-91
ATTORNEY/AGENT INFORMATION:
FELECOMMUNICATION NUMBER: 33,229
TELECOMMUNICATION NUMBER: 31,229
TELECOMMUNICATION NUMBER: 31,229
TELECOMMUNICATION INPORMATION:
FELECHONE: (215) 568-3109
INFORMATION FOR SEC IN NO: 1:
ELNGTH: 14255
TYPE: nucleic acid
SEQUENCE CHARACTERISTICS:
LENGTH: 14255
TYPE: nucleic acid
TYPE: No. 11 near
ANTI-SENSE: NO. 11 near
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,392
FILING DATE:
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158.50
32.17%
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Best Local Similarity:
Query Match:
DB:
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3	2077 GASSGIIGCCAGCCICCIAAAAAGGCCAAAGCICAGCTCTGCAAGATTGAGAAGAGTAA 2936
ò	lnLysGlnŢh 15
d d	 CACAGGGTCAAGAAAGTGACTCATC
ò	152 rAsnileGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr 172
g	2997 CTCTGTGCGAGGACCCCCGGATTAAACATGTCTGCAGAAGAGCAGCTGTTGCCCTTGGCCG 3056
ò	172 pGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTy 192
qq	3057 AAAACGAGCTGTGTTTCCTGATGACATGCCCACCCTGAGT3096
ò	192 rTyrlleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLy 212
qq	1
δ	212 aLysAlaLysValileAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSe 232
q d	3114 ACGAGAAAAGATTTTGTCTTCCATGGGGAATGATGACAGACA
ò	232 rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr 252
QQ	
ò	252 oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy 272
Ωp	3216 fGTCACTAGAAA 3227
ò	272 sAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuva 292
Q	3228 CAAGGCACCCCCAGAACCTCCAGTAAAGAAAGGACGTCG-ATCGAGGCGGT 3277
δ	292 lrrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArglleValSerTrpTrpMetTh 312
Q	33
ò	312 rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLygPh 332
g	3326 CTAATTGCTTAGATAAGCCCAAGTTTGGTGGTGGTGGAATATAAAGA 3370
ò	332 eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPh 350
g	TCAGA
ò	350 eHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlalleTyrGluValLeuGl 370
С	3431 TGCAGAAGCAAGCTAAAGCTGTGAAAA-AGAAAGAGAAAAAGTCTAAGACCAGTGAAAAG 3489
ò	370 nValAlaSerSerArgala 376
q	3490 AAAGACAGCAAAGAGAGTGTTGTGAAGAACGTGGTGGACTCTAGTCAGAAACCTACC 3549
ò	377GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGlyLy 393
QD	3550 CCATCAGCAAGAGGATCCTGCCCCAAAG-AAAAGCAGTAGTGAGCCTCCTCCACGAAA 3608
ò	393 sAlavalGluValGlnAenLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSe 413
Q	3609 GCCCGTCGAGGAAAAAGAGTGAAGAAGGGAATGTCTCGGCCCC 3650
ò	413 rGlyProLysGlyLeuGlu 419
^업	3651 TGGGCCTGAATCCAAACAGGCCACCACTCCAGGAAGTCAAGCAAG
ογ	420ProProGluGluGluLysAsnProTyrLysGluVa 431
Ор	AAG
ò	ITyrThrAspMetTrpValGluProGluAlaAlaTy
q	3771 TCCCAAAACCACTCCTAGTGAGCCCAAGAAAAGCAGCCTCCACCACAGAATC 3824

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                                                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/08306691B Patent No. 5734039
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Calabrett
APPLICANT: Skorski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4389
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                  SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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 APPLICATION NUMBER:
                                                 OPERATING SYSTEM: MS-DOS
                                                                                                                                          COUNTRY:
                                                                                                                                                                                           STREET:
                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTCCAGAGCAGAGCAAACAGAAAAAAGTGGCTCCCCGCCCAAGTATCCCTGTAAAACA 3884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTCCACAGGATCAGAGTGGACTTTAAGGAGGATTGTGAAGCAGAAAATGTGTGGGAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAACCAAAAGAAAAAGGAAAAACCACCTCCGGTCAATAAGCAGGAAGAATGCAGGCACTTT 3944
                                                                                                                                                                                                                                                                                                                                                                                                                                         GGATGCACAGTGGTCTCATGATTTCTCACTGTGTCATGAT 4488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pProSerArgLeuGlnMetPhePheAlaAsnAsnHisAsp 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCTGTACCAAGTGTGTTCGCTGTAAGAGCTGTGGATCCACAACTCCAGGCAAAGGGTG
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                                                                                                                                                                         SSEE: Seidel, Gonda, Lavorgna & Monaco,
T: Two Penn Center, Suite 1800
Philadelphia
                                                                                                                         19102
                                                                                                                                                          Pennsylvania
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                                                                                                                                                                                                                                                                                                                   Calabretta, Bruno
                                                                   IBM PS/2
                                                                                   Diskette, 3.50
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ANTISENSE
OLIGONUCLEOTIDES TARGETING
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US/08/306,691B
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14255 base pai
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REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Septemb
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2464
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: (215) 568-5549
rAsnIleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr
                                             GAGTCTTAAACAAACCGACCAGCCCCAAAGCACAGGGTCAAGAAAGTGACTCATCAGAGAC
                                                                                                            GAGGGTTGCCAGCCTCCTAAAAAAAGGCCAAAGCTCAGCTCTGCAAGATTGAGAAGAGTAA
                                                                                                                                                                        ATCCCTGGAGAAGGAGAAAACCCTCTGCCTTTCCACTCCTTCATCTAGCACTGTTAAACA
                                                                                                                                                                                                                                                                    AlaGluGlyGluGlyThrGluThrProPro----
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Matches:
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r 2 0	rTyrileSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLy 212	SLysalaLysValIleAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSe 232 :::: ::::::: ACGAGAAAAGATTTTGTCTTCCATGGGGAATGATGACAAGTCATCAATTGCTGGCTCA 3171	rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr 252	oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy 272 	3227	BAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGly11eGlyGluLeuVa 292 	TrpGlyLyBLeuArgGlyPheSerTrpTrpProGlyArglleValSerTrpTrpMetTh 312 	AlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLyaPh	TTAGATAAGCCCAAGTTTGGTGGTCGCAATATAAAGA 3370	eServalValcysValGluLysLeuMetProLeuSerSerPheCysSerAlaPh 350 	eHisGlnalaThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGl 370 	nValAlaSerSerArgAla376 : :::	caaagägäggagtgttgtgaagaacgtggtggactctagtcagaaacctacc 3549	GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGlyLy 393 	SAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSe 413 		TÓGGCCTGAATCCAAACAGGCCACCACTCCAGGTTCCAGGAAGTCAAGCAAG		TyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProProAlaLy 451	CCACTCCTAGTGAGCCCAAGAAAAAGCAGCCTCCACCACAGAATC 3824	1 : : : : : : : : : : : : : : : : : : :	uLysProLysValLysGlu
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Sequence 1, Application US/08545860D
Parent No. 6040140
Parent No. 6040140
Parent No. 6040140

GENERAL INFORMATION:
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz & ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz & CREST.
CITY: Philadelphia
                                                                                                                                  4005 AGTCCACAGGATCAGAGTTTTAAGGAGGATTGTGAAGCAGAAAATGTGTGGGAGAT 4064
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3945 GAACATCCTCAGCACTCTCTCCAATGGCAATAGTTCTAAGGAAAAAATTCCAGCAGATGG 4004
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                                                                                                                                                                                                                                                                                            493 sGlySerLeuAsnValThrLeuGluHisProLeuPhelleGlyGlyMetCysGlnAsnCy 513
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                                                                                             473 ----GluargLeuValTyrGluValArgGlnLysCys-----ArgAsnIleGluAsp-- 488
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COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN R-DOS/MS-DOS
SOFTWARE: PATENTIN BATH:
APPLICATION NOWER: US/08/545,860D
CLASSIPICATION NOWER: 1996
CLASSIPICATION DATA:
APPLICATION NOWER: PCT/US94/04496
FILING DATE: 22-APP-1994
PRIOR APPLICATION DATA:
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466 ----IlelleAspGluArgThrArg-------
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; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; ANTI-SENSE: NO US-08-545-860D-1
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1425
TYPE: nucleic acid
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PRIOR APPLICATION NUMBER: US 07/971,094

PILING DATE: 30-OCT-1992

PRIOR APPLICATION NUMBER: US 07/888,839

PILING DATE: 27-MAY-1992

PRIOR APPLICATION NUMBER: US 07/888,839

FILING DATE: 11-DEC-1991

APPLICATION NUMBER: US 07/805,093

PILING DATE: 11-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: DELUCA Esq., Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1262

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-0CT-1994
2757 ATCCCTGGAGAAAGGAAAACCCTCTGCCTTTCCACTCCTTCATCTAGCACTGTTAAACA 2816
                                                                                                                                                                                                                                            2584 TCATCTTCTGCCAAA-----AAAGCAACAGGGCGGAAGAAGTCTTCATCACATGATTCT
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                             113 AlaGluGlyGluGlyThrGluThrProPro--------
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FILING DATE: 11-OCT-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 ArgGlyLysGluGluArgGlnGlu---------ProserAla 40
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FILING DATE: 09-DEC-1992
                                                                            TATAAAGAAAGGGAGAGGAAATCTGGAAAAAACCAACTTGGACCTCGGCCCCAACTGCCCC 2756
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413 rGlyProLysGlyLeuGlu	S S	
393 sAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSe	유 성	
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252 oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy	Ş	
232 rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr	5 S	
212 sLysAlaLysValIleAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSe :::: :::::::: ::::::::::	dd Qy	
192 TIYTI1eseTLYSATGLYSATGASPGIUTTPLEUALAATGITPLYBATGGIUH1 	. מל	
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152 rAsnileGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr	B 성	
142SeralaGlyGluGlyLys-GluGlnLysGlnTh	Qy dd	
130 AsnG1yCysCysValThrLysG1uG1yArgG1yAla	В Q	
2817 TTCCACTTCCTCCATAGGCTCCATGTTGGCTCAGGCAGACAAGCTTCCAATGACTGAC	дд	
123GluAlaSerArgAlaValGlu	Ş	

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Sequence 1, Application PC/TUS9404496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcook Washburn, Kurtz, Mackiewitz &
ADDRESSEE: Woodcook Washburn, Kurtz, Mackiewitz &
CORRESPENTION: Oberies
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----ProProGluGluGluLysAsn-----ProTyrLysGluVa 431
                                                                                                  431 lTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProAlaLy 451
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::: |||:::||||:::||2404 GCTGACAAGAGAAGAAGAAGAGAGAGAGAGAAGAGAAAAGGAG 2463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2757 ATCCCTGGAGAAGGAGAAAACCCTCTGCCTTTCCACTCCTTCATCTAGCACTGTTAAACA 2816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2464 AATAAGCGGGAGTCAAGGAAAGAGAAAAGGAAAAAGGGATCAGAAATTCAGAGTAGTTCT 2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2524 GCTTTGTATCCTGTGGGTAGGGTTTCCAAGGAGGTTGTTGGTGAAGATGTTGCCACT 2583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2584 TCATCTTCTGCCAAA-----AAAGCAACAGGGGGAAGAAGTCTTCATCACATGATTT 2637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2697 TATAAAGAAAGGGAGAGGAAATCTGGAAAAACCAACTTGGACCTCGGCCCAACTGCCC 2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 ArgSerGluProGlnProGluGluGlySerProAlaAlaGlyGlnLyaGlyGlyAlaPro 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 AlaGluGlyGluGlyThrGluThrProPro---------------------------122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 -----GludlaSerArgAlaValGlu 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SerAlaGlyGluGlyLys-GluGlnLysGlnTh 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 ThrAlaArgLysValGlyArgProGlyArgLysArg---LysHisProProValGluSer 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 SerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGlnAspSer 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GlyPro-------SerAspLeuLeuProAsnGlyAspLeuGluLys 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SerSerSerSerLeuGluArgGluAspArgLysGluGlyGluGluGluGluAsn 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 AsnGlyCysCysValThrLysGluGlyArgGlyAla--------
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-720-086-5 (1-908) x PCT-US94-04496-1 (1-14255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                               FILING DATE:
CLASASIFACATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Beg., Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TJU-1242
TELEPHONE: (215) 568-3100
ITELEPAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US94-04496-1
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
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:G1 459 ;;	451 sLysProArgLysSerThrThrGl	δ
TC 3824	431 TyrThrAspMetTrpValG uProG uAlaAlaAlaTyrAlaProProProProProAlaLy	25 3 67
GT 3770	711 CCAGCCAGCACTGGTCATCCCGCCTCAGCCACCTACTACAG	w
'n	651 TGGGCCTGAATCCAAACAGGCCACCACCTCCAGCTTCCAGGAAGTCAAGCAAG	0 5
- 419	413 rGlyProLysGlyLeuGlu	
CC 3650	3609 GCCCGTCGAGGAAAAGAGTGAAGAA	Db 3
Se 413	393 sAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProS	γQ
ω	550 CCATCAGCAAGAGAGGATCCTGCCCCAAAG-AAAAGCAGTAGTGAGCCTCC	ω
у зэз	377GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGlyLy	δ
C 35	490 AAA	ω
176 176	PHOLINGHANGCHANGCIAAANGCIGIGAAAAAAAAAAAAAAAAAAAAAAAAA	Ş
1 370	50 eHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAl	
CC 3430	371 AGCAGTGCTGCAAGATGAGAAAAT	Db 3
Ph 350	/alCysValGluLysLeu-	γQ
ωι		W
 	312 rGlvårgserårgålaålaGluGlvmhrårgTrnVa	
Th 312	292 TrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMetTh :::	음 성
 GT 3277	3228 CAAGGCACCCCAGGAACCTCCAGTAAAGAAAGGAACGTCG-ATCGAGGCGGT	Db 3
Va 292	272 sAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuVa	ş
AA 3227	3216 TGTCACTAGAAA	Db 3
Ly 272	252 oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy	Ş
CC 3215	172GAAGATGCTGAACCTC	Db 3
Pr 252	232 rGlnLysValGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerP	δ (
3171	bild ACGAGAAAAGATTTTGTCTTCCATGGGGAATGATGACAAGTCATCAATTGCTGGCTCA-	
)	010 01 100 101 101 101 101 101 101 101	
Ly 212 ::	192 rTyrileSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLy	음 성
3096	057 AAAACGAGCTGTGTTTCCTGATGACATGCCACCCTGAGT	ω
Ty 192	172 pGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTy	δ
CG 3056	2997 CTCTGTGCGAGGACCCCGGATTAAACATGTCTGCAGAAGAGCAGCTGTTGCCCTTGGCCG	<u>Db</u> 2
Tr 172	152 rAsnileGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr	Ş
 AC 2996	::: 2937 GAGTCTTAAACAAACCGACCAGGCCCAAAGCACAGGGTCAGGAAAGTGACTCATCAGAGAC	Db 2

	AFFLICATION NUMBER: US/US/USU,255 FILING DATE: 1993617 CLASSIFICATION: 435	CEF	·. ·. ·.
	ON DATA:	CURR	., .
	SYSTEM: PC-DOS/MS-DOS	999	
	TYPE: Fl	6 F	
	ZIP: 77210 COMPUTER READABLE FORM:	COME	
	Ľ	8	. , .
	CITY: Houston STÀTE: Texas	SI CI	·· ··
	P. O. Box 4433	I.S.	
	CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, White & Durkee	AL AL	
	OF SEQUENCES:	NUMBER	
	OF INVENTION: TRANSLOCATIONS	TITLE	٠
	OF INVENTION:	STILLS STILLS	·· ··
	CANT: Diaz, Manuel O.	APPL	
	NERAL INFORMATION: APPLICANT: Rowley, Janet D.	GENERA APPL	
	0-255-4 20-255-4 20-4, Application US/08080255 No. 5487970	S-08-080-2 Sequence Patent No	··· 52
	9 GGATGCACAGTGGTCTCATGATTTCTCACTGTGTCATGAT 4488	444	ДĎ
		y 597	δ
4448	GATCTGTACCAAGTGTGTTCGCTGTAAGAGCTGTGGATCCACAACTCCAGGCAA	0 4389	ДD
597	PASNCYSTYrMetCYSGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgAluAspTr	1 577	ફ
4388		0 4341	Ωb
577	sValAspLeuLeuVa	/ 558	Ş.
4340	TACAAAGCAGCTGCTGGAGTGTAATAAGTGCCGAAACAGCTATCACCCTGAGTG	0 4287	뭣
558	-G1	/ 539	Ş
4286		0 4227	Dβ
538	3 yTyrGlnSerTyrCysThrIleCys	/ 528	Ş
4226		0 4167	뮰
528	ş	/ 513	Ş
4166		0 4125	타
513	sGlySerLeuAsnValThrLeuGluHisProLeuPheIl	/ 493	Ş
4124	<pre>5 GGGAGGCTTAGGAATCTTGACTTCTGTTCCTATAACACCCAGGGTGGTTTGCTTTCTCTG</pre>	0 4065	đg
493		489	Q
4064	AGTCCACAGGATCAGAGTGGACTTTAAGGAGGATTGTGAAGCA	0 4005	da da
488	GluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAsp	473	Ş
4004	; ; GAACATCCTCAGCACTCTCTCCAATGGCAATAGTTCTAAGCAAAAAATTCCAGCAGATGG	3945	멍
472	5IleIleAspGluArgThrArg	466	S S
3944	: ;	3885	밁
465		459	γQ
3884	AGGTCCAGAGCAGAGCAAACAGAAAAAAAGTGGCTCCCCGCCCAAGTATCCCTGTAAAACA	3825	뫄

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850 CTCTGTGCGAGGACCCCGGATTAAACATGTCTGCAGAAGAGCAGCTGTTGCCCTTGGCCG 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 GGGACTGATATTACTTCTGTGACTCTTGGGGATACAACAGCTGT-CAAAACCAAAATACT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 ArgSerGluProGlnBroGluGluGlySerProAlaAlaGlyGlnLysGlyGlyAlaPro 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550 TATAAAGAAAGGGAGAGGAAATCTGGAAAAACCAACTTGGACCTCGGCCCAACTGCCCC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 AlaGluGlyGluGlyThrGluThrProPro---------------- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    610 ATCCCTGGAGAAGGAGAAAACCCTCTGCCTTTCCACTCTTCATCTAGCACTGTTAAACA 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 -----GluAlaSerArgAlaValGlu 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 rAsnileGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 pGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTy 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 .....serAlaGlyGluGlyLys-GluGlnLysGlnTh 152
                                                                                                                                                                                                                                                                                                                                                                                                                                   60 SerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGlnAspSer 79
                                                                                                                                                                                                                                                                                                                                                                            10 SerSerSerSerLeuGluArgGluAspArgLysGluGlyGluGluGluGluAsn 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 GlyPro------SerAspLeuLeuProAsnGlyAspLeuGluLys 92
                                                                                                                                                                                                                                               4201
148
105
274
211
                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                  US-09-720-086-5 (1-908) x US-08-080-255-4 (1-4201)
ATTORNEY/AGENT INFORMATION:
NAME: PERKEY. David L.
REGISTRATION NUMBER: 32.165
REFERENCE/DOCKET NUMBER: ARCD:072/PAR
TELECOMMUNICATION INFORMATION:
TELETRAX: (512) 320-720
INFORMATION FOR EDG ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4201 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
                                                                                                                                                                           ; TOPOLOGY: linear;
; MOLECULE TYPE: DNA (genomic)
US-08-080-255-4
                                                                                                                                                                                                                                          0.00427
157.00
34.47%
20.16%
3.20%
                                                                                                                                                                                                                                                              Percent Similarity: 3
Best Local Similarity: 2
Query Match: 3
DB:
                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
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ò	192	rTyrIleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLy	212
d d	950	: :	996
ò	212	SLysAlalysValileAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSe	232
q	967	ACGAGAAAAGATTTTGTCTTCCATGGGGAATGATGACAAGTCATCAATTGCTGGCTCA	1024
ò	232	rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr	252
qq	1025		1068
δλ	252	oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy	272
đ	1069	TGTCACTAGAAA	1080
ò	272	sAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuVa	292
g	1081	CAAGGCACCCCAGGAACCTCCAGTAAAGAAAGGACGTCG-ATCGAGGCGGT	1130
ò	292	1TrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArg1leValSerTrpTrpMetTh	312
QQ	1131	dradacaororoccidecraccadaraccraagacraticara	1178
ò	312	rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLyBPh	332
qq	1179	CTAATTGCTTAGATAAGCCCAAGTTTGGTGGTCGCAATATAAGA	1223
ò	332	eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAl	349
ор	1224	AGCAGTGCTGCAAGATGAAAATGTCAGAATCTACTACAATGGATGCCTTCCAAAGCCT	1283
ò	349	aPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLe	369
DÞ	1284	ACCTGCAGAAGCTAAAAGCTGTGAAAA-AGAAAAGAGAAAAAAGTCTAAGACCAGTGAA	1342
ò	369	uGlnValAlaSerSerArgAla	376
Op	1343		1402
ò	377	GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGl	392
엄	1403	ACCCCATCAGCAAGAGGGATCCTGCCCAAAG-AAAAGCAGTAGTGAGCCTCCTCCACG	1461
ò	392	yLysAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnPr	412
g	1462	AAAGCCCGTCGAGGAAAAGAGTGAAGAA	1503
ò	412	oSerGlyProLysGlyLeuGluProProGluGluGluLysAanProTyrLysGl	430
q	1504	AATC	1563
ò	430	uValTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProPro	447
g	1564	CTCCCAGCCAGCACTGGTCATCCCGCCTCAGCCACCTACAGG	1608
ò	448	-ProProAlaLysLysProArgLysSerThrThrGluLysProLysValLys	464
g	1609	ACCGCCAAGAAAGAAGTTCCCAAAACCACTCCTAGTGAGCCCCAAGAAAAGCAGCCTCC	1668
ò	465	GluilelleAspGluArgThrArgGluArgLeuValTy	477
đ	1669	ACCACCAGAATCAGGTCCAGAGCAGAGCAAACAGAAAAAAAA	1728
λö	477	rGluValArgGlnLysCysArgAsnIleGluAspIleCysIleSe	492
QQ	1729	CCCTGTRABACABABACCBABABABABABABABACCACCTCCGGTCABTABCCAGGAGA	1788
ò	492	rCysGlySerLeuAsnValThrLeuGlu	501
qq	1789	: : : : : :	1848

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; TOPOLOGY:
; MOLECULE TYI
US-08-465-713-4
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; Patent No. 6121419
; GENERAL INFORMATION:
APPLICANT: Rowley, Ja
APPLICANT: Diaz, Manu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-465-713-4
                                                                 TELEPHONE: (512) 320-7200
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4201 base pairs
TYPE: nucleic acid
GTBANNEDNESC CALL
                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/0
FILING DATE: 17 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS
TITLE OF INVENTION: TRANSLOCATIONS
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                                                                                                                                                                                  NAME: Patker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                      STRANDEDNESS:
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oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLySAsnAlaThrLy 272
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                                                                                                                                                                                                                                                                                                                                           rAsnIleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr 172
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                                                                 rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr 252
                                                                                                     ACGAGAAAAGATTTTGTCTTCCATGGGGAATGATGACAAGTCATCAATTGCTGGCTCA--
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                                 -GAAGATGCTGAACCTCTTGCT-----CCACCCATCAAACCAATTAAACC 1068
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Indels:
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Conservative:
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q	1069	TGTCACTAGAAA	1080
ò	272	SAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuVa	292
g	1081	aaggacgtcg-atcgaggcgg	1130
ò	292	TrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArglleValSerTrpTrpMetTh 	312
g	1131	ĠTĠĠĠĊAĞTĞTÇÇÇĞĠCTĞÇĞÄĞĞTĞCTĞAĞĞACTĞTĞTĞTŢTĞTA	1178
ò	312	rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLysPh	332
οp	1179	CTAATTGCTTÄĞATAAĞCCCAAGTTTGGTGGTCGCAATATÄÄĞA	1223
ેં	332	eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAl	349
e G	1224	AGCAGTGCTGCAAGATGAAAATGTCAGAATCTACTACAATGGATGCCTTCCAAAGCCT	1283
ò	349	aPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLe	369
g	1284	acctgcagaagcaaagctgtgaaaa-agaaagagaaaagtctaagaccagtgaa	1342
કે	369	uGlnValAlaSerSerArgAla	376
g	1343	AAGAAAGACAGCAAAGAGAGTGTTGTGAAGAACGTGGTGGACTCTAGTCAGAAACCT	1402
ે	377	GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGl	392
q	1403	ACCCCATCAGCAAGAGGATCCTGCCCAAAG-AAAAGCAGTAGTGAGCCTCCTCCACG	1461
ò	392	yLysAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnPr	412
QQ	1462	AAAGCCCGTCGAGGAAAAGAGTGAAGAA	1503
ò	412	oSerGlyProLysGlyLeuGluProProGluGluGluGluIysAsnProTyrLysGl	430
g	1504	ccredectreaarccaaacaecaccacrecteaacrrccaagaagrcaagcaagr	1563
કે	430	Ala	447
QQ	1564	CTCCCAGCCAGCACTGTCATCCCGCTCAGCCACCTACTAGG	1608
ò	448	-ProProAlaLysLysProArgLysSerThrThrGluLysProLysValLys	464
qq	1609	acceccaaaaaaaaarreccaaaaccacrecragreaccaaaaaaaaaccrec	1668
ò	465	GlullelleAspGluArgThrArgGluArgLeuValTy	477
g	1669	ACCACCAGATCAGGTCCAGAGCAGAGCAGAAAAAAAAGGCTCCCCGCCCAAGTAT	1728
ò	477	rGluValArgGlnLysCysArgAsnIleGluAspIleCysIleSe	492
g	1729	CCCTGTAAAACAAAAACCAAAAAGAAAAAGGAAAAAACCACCTCCGGTCAATAAGCAGGAGAA	1788
ò	492	rCysGlySerLeuAsnValThrLeuGlu	501
qq	1789	:	1848
ò	502		513
g	1849	rccagcagargagrccacagarcagagrgagrtraagrrrgrgrarrdccaagrcrd	1908
6	513	8	528
g	1909	Trergagecerrecacadarrrretrragagadaaacgagecerergagadaecager	1968
ò	528	yTyrGlnSerTyrCysThr11eCysCysGly	538
g	1969	GGAAAATTGGTGTTGTCGTTGCAAATTCTGTCACGTTTGTGAGGAAGGCAACATCAGGC	2028
ò	539	-GlyargGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGluCy	558
g	2029	TACAAAGCAGCTGCTGGAGTGTAATAAGTGCCGAAACAGCTATCACCCTGAGTG	2082

Search completed: November 25, 2002, 01:45:03 Job time : 312.239 secs

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Mon Nov 25
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Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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US-09-665-309-1 US-09-661-569-1 US-08-455-633A-35 US-08-416-336-5 US-08-416-336-5	-09-461- -08-445- -08-170- -08-447- -08-445- -09-416-	US-09-370-473-5 US-09-370-473-5 US-09-813-818-1 US-08-520-678A-30 US-08-897-126-30	-08-232-463-1 -09-333-423-1 -09-091-097-7 -08-361-467808-484-332C09-196-390-1 -09-149-476-2 -09-149-476-2	ID US-09-276-531-47 US-08-232-463-14
Sequence 1, Appli Sequence 1, Appli Sequence 35, Appli Sequence 35, Appli Sequence 5, Appli Sequence 35, Appli	. L. a. a. a. L.	Sequence 29, Appl Sequence 5, Appli Sequence 1, Appli Sequence 30, Appl Sequence 30, Appl	122144711	Description Sequence 47, Appl Sequence 14, Appl

29 40.2 1.0 1100 3 US-09-248-335-53 30 40.2 1.0 1466 4 US-08-984-919A-10 31 40.2 1.0 1466 4 US-08-984-919A-12 32 40.2 1.0 1472 4 US-08-781-420-10 33 40.2 1.0 1472 4 US-08-781-420-12 34 40.2 1.0 1472 4 US-08-874-102-12 35 40.2 1.0 1472 4 US-08-874-102-12 36 40.2 1.0 1472 4 US-08-874-102-12 37 40.2 1.0 1472 4 US-08-874-102-12 38 40.2 1.0 1472 4 US-09-06-995A-10 37 40.2 1.0 1472 4 US-09-06-995A-12 38 40.2 1.0 1472 4 US-09-06-995A-12 39 40.2 1.0 1472 4 US-09-06-995A-12 39 40.2 1.0 1472 4 US-09-06-995A-12 39 40.2 1.0 1875 4 US-08-984-919A-46 40 40.2 1.0 1881 4 US-08-984-919A-46 41 40.2 1.0 1881 4 US-08-874-102-46 42 40.2 1.0 1881 4 US-08-874-102-46 43 40 1.0 2852 3 US-09-027-137-2 44 40 1.0 2852 3 US-09-032-684-11				Ω		ი			ი		ი		Ω		Ω			
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3 US-09-248-335-53 4 US-08-984-919A-10 4 US-08-984-919A-12 4 US-08-781-420-10 4 US-08-781-420-12 4 US-08-781-420-12 4 US-08-781-420-12 4 US-08-874-102-12 4 US-09-006-595A-10 4 US-09-006-595A-10 5 34034-5 6 534034-5 6 US-08-984-919A-46 4 US-08-984-919A-46 4 US-08-984-919A-46 6 US-08-984-919A-46 6 US-08-984-919A-46 7 US-08-984-919A-46 8 US-08-984-919A-46 9 US-08-984-919A-46 9 US-08-984-919A-46 9 US-08-984-919A-46 9 US-08-984-919A-46 9 US-08-984-919A-46 9 US-08-984-919A-46 9 US-08-984-919A-46 9 US-08-984-919A-46 9 US-08-874-102-46 9 US-08-874-102-46 9 US-08-874-102-46 9 US-08-874-102-46 9 US-09-344-441-2	337	2852	2852	1881	1881	1875	1875	1493	1472	1472	1472	1472	1472	1472	1466	1466	1100	
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	US-09-032-684-11	US-09-344-441-2	US-09-027-137-2	US-08-874-102-48	US-08-874-102-46	US-08-984-919A-48	US-08-984-919A-46	5340934-5	US-09-006-595A-12	US-09-006-595A-10	US-08-874-102-12	US-08-874-102-10	US-08-781-420-12	US-08-781-420-10	US-08-984-919A-12	US-08-984-919A-10	US-09-248-335-53	
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53 110 110 110 110 110 110 110 110 110 11	Appl	Appli	Appli	App1	App1	Appl	App1	5340934	Appl	Appl	Appl	App1	App1	Appl	Appl	App1	Appl	

ALIGNMENTS

		RESULT US-09- Sequ Pate Pate A A A A A A A A A A A A A A A A A A A
FILING DATE: MATCH 27, 1998 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Lynn E. MUXTY, Ph.D. REGISTRATION NUMBER: 42,918 REPERENCE/DOCKET NUMBER: PA.0008 US TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 855-0555 TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO: 47: SEQUENCE CHARACTERISTICS: LENGTH: 2077 base pairs TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: TESTTUTO2	NUMBER OF SEQUENCES: 134 CORRESPONDENCE ADDRESS: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALLFORNIA COUNTRY: USA ZIP: 94304 COMPUTER REALABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION NUMBER: US/09/276,531 FILING DATE: Herewith CLASSIFICATION: BATA: APPLICATION HATA: BEDS! CATTON NUMBER: US/09/276,531 PRIOR APPLICATION DATA: BEDS! CATTON NUMBER: US/09/276,531 PRIOR APPLICATION DATA:	11 276-531-47 ence 47, Application ence 47, Application nt No. 6183968 ERAL INFORMATION: PPLICANT: Bandman, C PPLICANT: Lal, Preet PPLICANT: Hillman, J PPLICANT: Reddy, Roo PPLICANT: Guegler, K

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3301 CATTTGCTGGAGGATGCTATTGTGAATGTGGGCTCAGATGAGCCAAGGTCAAGGGGCCAAA 3360
                                                                                       3361 AAAAATTCCCCCTCTCCCCCCAGGAGTATTTGAAGATGATGTTTATGGTTTAAGTCTTCC 3420
                                                         1065 TGTTTACAGACGTGTGCAGTTGTAGGCATGTACAGGACATTTTTAAGGGCCCAGGA 1124
1018 G-----ACAGTTATTGCAAGAGTTTAATTTTTGAAAACTGGCTACTGCTCTG 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGCCTGTGAATAGTICTACCCAGGACTGGGGAGCTCTCG-----GICAGAGCCAGTG 2887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  958 ACCAÁAACCACAGTGCCGACAGCTCTCCAATACTCAGGTTAATGCTGAAAATCATCCAA 1017
                                                                                                      2295 GGCTCTTCTTCGAGTTTTACCACTTGCTGAATTATACCCGCCCCAAGGAGGGCGACAACC 2354
                                                                                                                                                                2475 ACAGGGCCCGGTACTTCTGGGGTAACCTACCGGAATGAACAGGCCCGTGATGGTTTCAA 2534
                                                                                                                                                                                                                                                                                                                                                AGAATGATAAGCTCGAGCTGCCTGGAGTTCAGTAGGACAGCAAAGTTAAAGA 2594
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                                        13.1%; Score 548.4; DB 4; Length 2077; 71.4%; Pred. No. 1.8e-144; Indels 49; Gaps. ive 0; Mismatches 306; Indels 49; Gaps.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    777
                                                                                                                        65 GGCTCTTCTTCGAATTTT-CCACCTGCTGAATTACTCACGCCCCAAGGAGGTGATGACC 123
                                                                                                                                                                                                                                                                                                                 244 ACAGGGCCCGATACTTCTGGGGCAACCTACCCGGGATGAACAGGCCCGTGATAGCATCAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 GGNCGTTCTTCTGGATGTTTGAGAATGTTGTAGNCTCGTGCCGATTCGGCAGAGGGACA
                                                                                                                                                                                                                                                                                                                                                                  364 AAGTACAGACAATAACCACCAAGTCGAACTCGATCAAACAGGGGAAAAACCAACTTTTCC
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                                                                                                                                                                                                                        2415 TCTCAAGATTCCTGGCATGTAACCCAGTGATGATCGATGCCATCAAGGTGTCTGCTGCTC
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                                         Query Match
Best Local Similarity 71.4'
Matches 888; Conservative
 ; CLONE: 1271435
US-09-276-531-47
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3421 TGGCACCTTCCCCTTGCTTTGGTACAAGGGCTGAAGTCCTGTTGG------TCTTGTAG 3473
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1125 TCGTTTTTTCCCAGGGAAGCAGAAG----AGAAAATGTTGTATATGTCT----TTTACC
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                                                                                                                                                          3474 CATTICCCAGGAIGAIGAIGICAGCAGGGAIGACAICACCACC 3516
                                                                                                                                                                                        STATE: VA.
COUNTRY: USA
ZIP: USA
ZIP: USA
ZIP: 22313-0299
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Factor No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
AMARE: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STRANDEDNESS: sin
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IMMEDIATE SOURCE:
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                                                                                              APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                  ZIP: 22313-0299

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
                                                        TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1060 AGCTCCCTCGACC 1048
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1180
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTCCTTCCACC 1625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCGTCGTTCAGACAGTAGGAACTTAGAACCCAGGAGACGCGAGAACAAAAGTCGAAGA 1432
                       1: 7218 base pairs nucleic acid
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linear
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Best Local Similarity
Marches 17; Conserva
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; CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                                                       US-09-333-423-1
                                                                       Query Match
Best Local
                                                                                                                                                                                                                              SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09333423 Patent No. 6265636
                                                                                                                                                                                                                                                                    FILE REFERENCE: 0818
CURRENT APPLICATION NUMBER: US/09/333,423
CURRENT FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,998
EARLIER FILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Randall, Douglas
APPLICANT: Thelen, Jay
APPLICANT: Miernyk, Jan
APPLICANT: Muszynski, Michael
APPLICANT: Sewalt, Vincent
                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Pyruvate Dehydrogenase Kinase TITLE OF INVENTION: Polynucleotides, Polypeptides
                                                                                                                                ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (55)...(1095)
                                                                                                                                                                                                 TYPE: DNA
                           3128 GATGGCTTTCTTTTACCCTCCTGAGTTTATCACTCAGAAGTGATGGCTAAGATACCAAAA 3187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 45.2; DB nilarity 4.3%; Pred. No. 0.035; Conservative 212; Mismatches
                                                          Conservative
                                                                       1.0%;
                                                         0
                                                                       Score 43.2; DB 4; Pred. No. 0.047;
                                                          Mismatches
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                                                                                     Length 1332;
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                                                 APPLICANT: Van Ermalo, John
APPLICANT: Van Ermalo, John
APPLICANT: Van Ermalo, John
APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Souza, Maria-Helena
APPLICANT: Van Montegu, Marc
TITLE OF INVENTION: EMBRYOS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           ADDRESSE:
ADDRESSE:
ADDRESSE:
BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STRATE: Virginia
COUNTY: United States
CONFUTRY: UNITED STATES
APPLICATION NUMBER: US 07/681,492
FILING DATE: 04-ARR-1991
PRICE APPLICATION NUMBER: US 07/681,492
FILING DATE: 04-ARR-1991
PRICE APPLICATION NUMBER: US 07/681,492
FILING DATE: 04-ARR-1991
PRICE APPLICATION NUMBER: US 09 402 224.3
FILING DATE: 04-ARR-1990
ATTORNEY/AGRATI THORNATION:
REPERENCE/DOCKET NUMBER: 01-AUG-1990
ATTORNEY/AGRATI THORNATION:
TELEFONNINICATION NUMBER: 01-AUG-1990
ATTORNATION NUMBER: 01-AUG-1990
ATTORNEY/AGRATI THORNATION:
TELEFONNINICATION NUMBER: 01-AUG-1990
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TELEFONNINICATION NUMBER: 01-AUG-1990
ATTORNEY/AGRATI THORNATION:
TELEFONNINICATION NUMBER: 01-AUG-1990
ATTORNEY/AGRATI THORNATION:
AGGRATICATION NUMBER: 01-AUG-1
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US-08-484-332C-4
; Sequence 4, Application US/08484332C
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TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: CDNA
| IMMEDIATE SOURCE:
| CLONE: 3C9
US-08-361-4678-4
Patent No. 5633441
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APPLICANT: TAKESAKO, KAZUTOH
APPLICANT: OKADO, TAKASHI
APPLICANT: OKADO, TAKASHI
APPLICANT: OKADIANA, MASANOBU
APPLICANT: KURODA, MASANOBU
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKTO, IKUNOSHIN
APPLICANT: AKTO, IKUNOSHIN
APPLICANT: AKTO, IKUNOSHIN
APPLICANT: AKTO, IKUNOSHIN
APPLICANT: YAMGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN
TITLE OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STRRET: PO BOX 747
CITY: FALLS CHURCH
GTTY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
                                     3188 AAACAAACAAAAACAGAAACAAAAAAAAAAAAAA 3223
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US-08-361-467B-4
; Sequence 4, Application US/08361467B
                                                                                                                                                               RESULT 5
US-09-091-097-7
; Sequence 7, Application US/09091097
; Patent No. 6432407
; GENERAL INPORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
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COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
TVPE: Floppy disk
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, LOCATION: 2..673
US-09-091-097-7
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INFORMATION:

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Best Local S
Matches 82
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APPLICANT:
APPLICANT:
                                                                                           3134
                                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 08/361,467
PRILING DATE: 22-DBC-1994
PRIOR APPLICATION NUMBER: US 07/681,492
APPLICATION NUMBER: US 07/681,492
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IMMEDIATE SOURCE:
CLONE: 3C9
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                             3194 ACAAAAACAGAAACAAAAAACAAAAAA 3221
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 04-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-AUG-1990 PRIOR APPLICATION DATA:
                                                                                                                           689
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TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                            EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 836-2021
ORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER: 010830-093
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                                                                                       CGTAGTTTTCTTGTTTTCTTTTCTCTCTATCAAAACCCAACAAGTAAAATGGA 948
AAAAAAAAAAAAAAAAAAAAAAAAAA 1036
                                                          82;
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                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                          nucleic
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                                                                                                                                                                                                                                                                                                                                                          1046 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Emmelo, John
De Oliveria, Dulce E.
De Souza, Maria-Helena
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States
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                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                    0; Mismatches
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US-09-196-390-1
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               Query Match
Best Local &
   Matches
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                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 596-90
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                     TOPOLOGY: Ilien.
MOLECULE TYPE: CDN
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APPLICATION NUMBER:
FILING DATE: 28-MAY-
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 36 917.7
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PRIOR APPLICATION NUMBER: DE 196 21 588.9
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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                                                                                                                       FEATURE:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                     ANTI-SENSE: NO ORIGINAL SOURCE:
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                                                                                    NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Haley, Jr., James F
REGISTRATION NUMBER: 27,7
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               Local Similarity
                                                                                                                                                                                                      STRAIN:
                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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Kossmann, Jens
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ive 0; Mismatches 73; Indels 0
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EARLIER PILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER PLING DATE: 1997-05-23
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EARLIER PILING DATE: 1997-04-11
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FILING DATE: 1997-08-22
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R APPLICATION NUMBER: 60/047,594

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,589

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,593
                                                                                                           RR APPLICATION NUMBER: 60/057,650
ER FILLING DATE: 1997-09-05
ER APPLICATION NUMBER: 60/056,884
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/057,669
ER FILLING DATE: 1997-09-05
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R APPLICATION NUMBER: 60/056,887
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/048,964
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/048,964
R FILING DATE: 1997-06-06
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,875
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FILING DATE: 1997-08-22
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/056,632
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/043,576
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
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APPLICATION NUMBER: 60/047,599
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APPLICATION NUMBER: 60/047,595
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APPLICATION NUMBER: 60/056,862
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Score 42; DB Pred. No. 0.11 0; Mismatches
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CURRENT FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-03-06
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EARLIER FALLING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-06-23
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EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-08-22
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0; Gaps ch 1.0%; Score 42; DB 4; Length 2323; 1 Similarity 60.5%; Pred. No. 0.14; 69; Conservative 0; Mismatches 45; Indels Query Match Best Local S Matches 69

3118 TAGGTAGTAAGATGGCTTTCTTTTACCCTCGAGTTTATCACTCAGAAGTGATGGCTAA 3177

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FILING DAIL.

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP HEI. 7/268700

FILING DATE: 17-0CT-1995

ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-43086
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-08-731-272A-29/c
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                                                                                          US-09-370-473-5
                                                                                                            RESULT 12
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Best Local S
Matches 61
Sequence 5, Application US/09370473
Patent No. 6271031
GENERRAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Apprin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)293-786
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID OF C TYPE HEPATITIS VIRUS USING TITLE OF INVENTION: DERIVATION AND PROCESS FOR DETECTION VIRUS USING TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3178
                                                                                                                                                                                               3223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tanaka, Torahiko
APPLICANT: Katoh, No. 5837463uyuki
APPLICANT: Shimotohno, Kunitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION,
                                                                                                                                                                                                                                   145
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 271 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01
FILING DATE: 11-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                 AGAAAAACAGTTAGCTATGGAGTGTAGCTAATG
                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                    Similarity 65.661; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W.
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                                                                                                                                                                                                                                                                                                                    1.0%;
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RESULT 14
US-08-520-678A-30/c
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                                                                                                                                                                                                                                                        Query Match
Best Local Sim
Matches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al
TITLE OF INVENTION: ISOLATED HUMAN CASEIN KINASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 2065
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
LENGTH: 2091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09813818 Patent No. 6448057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Quinolinate Metabolism Enzymes
FILE REFERENCE: BB-1209
CURRENT APPLICATION NUMBER: US/09/370,473
CURRENT FILING DATE: 1999-08-09
EARLIER PELICATION NUMBER: 60/096,240
EARLIER FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/813,818
CURRENT FILING DATE: 2001-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Triticum
                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                            3197
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mes 81; Conserv
                                                                                               CAAACAAAAACAGAAACAAAAAAAAAAAAAAACCTCAACA 3231
                                                                                                                                                             GGCTTTCTTTTACCCTCCTGAGTTTATCACTCAGAAGTGATGGCTAAGATACCAAAAAAA 3190
                                                                                                                                                                                            CCGCCCTGTACTCCCTGACGATTCCACTGTAACTACCAATCTTCTACTTGGT--TAAGAC 1980
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Pred. No. 0.2;
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Pred. No. 0.2;
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Sequence 30, Application US/08520678A Patent No. 5874565

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us-09-720-086-2.rni

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Mon Nov 25 08:18:10 2002
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Query Match
Best Local Similarity 67.9%; Pred. No. 0.088;
Matches 57; Conservative 0; Mismatches 27; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,126
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,678
FILING DATE:
APPLICATION NUMBER: 08/520,678
FILING DATE:
APTORNEY AGENT INFORMATION:
NAME: Henderson, Melodis W.
REGISTRATION NUMBER: 37,848
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 22, 2002, 09:19:58 Job time : 212.773 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 270 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-897-126-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Sequence 30, Application US/08897126
Sequence 30, Application US/08897126
Sequence 1 NPORMATION:

APPLICANT: Rice, Charles M.
APPLICANT: Rolykhalov Alexander A.
APPLICANT: Kolykhalov Alexander A.
TITLE OF INVENTION: O'NIUG GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF UNMERS OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO.
        GENERAL INFORMATION:

APPLICANT: Rice, Charles M.
APPLICANT: ROJYKALOV, ALexander A.
APPLICANT: KOJYKALOV, ALExander A.
APPLICANT: KOJYKALOV, ALEXANDER A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: Howell & Haferkamp, L.C.
ADDRESSE: Howell & Haferkamp, L.C.
STREET: ST. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 67.9%; Pred. No. 0.088;
Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6029-6836
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ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3236 TCTTAGTACTCAGGTTCATGCTGC 3259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37 848
REFERENCE/DOCKET NUMBER: 6029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5184
TELEPHONE: 314-727-5184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO. 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-678A-30
                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-08-897-126-30/c
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Minimum
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-MODEL-frame+_p2n.model -DEV=xlh
-MODEL-frame+_p2n.model -DEV=xlh
-MODEL-frame+_p2n.model -DEV=xlh
-MODEL-frame+_p2n.model -DEV=xlh
-MOPEXT=0 -IVSPTO_spool/US09720086/runat_18112002_092957_29457/app_query.fasta_1.4252
-DB-ISSued_Patents_NA -OPMT=fastap -SUPFTX=rni -MINNATCH=0.1 -I.OOFCL=0
-LOOPEXT=0 -UNITS-Bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE-pCt -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL-IOCAL -OUTFMT=pto -NORM-sct +HEARPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09720086_@CGN 1 1 108 @runat_18112002_092957_29457 -NCPU=6 -ICPU=3
-NO XLPXY -NO MMAP -LRAGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                          Result
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148.5
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146.5
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length: 2000000000
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Ygapop 10.0 , y
Fgapop 6.0 , E
Delop 6.0 , F
                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                        Match
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US-09-041-886-18

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ALIGNMENTS

US-09-276-531-47

Sequence 47, Application US/09276531 Patent No. 6183968

GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA: APPLICANT: CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA: NUMBER OF SEQUENCES: APPLICATION NUMBER: FILING DATE: March CLASSIFICATION: APPLICATION NUMBER: US FILING DATE: Herewith CITY: PALO ALTO STATE: CALIFORNIA STREET: CLASSIFICATION: ZIP: 94304 COUNTRY: 3174 PORTER DRIVE USA Lal, Preeti Hillman, Jer Reddy, Yue, Henry Bandman, NUMBER: 60/079,677 March 27, 1998 Roopa Olga Jennifer L. 134 US/09/276,531

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NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEFORM: (650) 845-4166
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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Best Local Similarity:
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US-09-276-531-47
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US-08-913-832A-1
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Sequence 1, Application US/08913832A
Patent No. 632917
GENERAL No. 632917
GENERAL TWOCRMATION:
APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFRENCE: 8484-0030-999
CURRENT APPLICATION NUMBER: US/08/913,832A
CURRENT APPLICATION NUMBER: PCT/DE96/00444
PRIOR PILING DATE: 1996-01-12
PRIOR PILING DATE: 1996-03-08
NUMBER OF SEQ ID NOS: 2
SOCTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1
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ORGANISM: Homo sapiens
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APPLICANT: Renz, Manted
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFERENCE: 8484-0059-999
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Percent Similarity:
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Patent NO. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
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CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 8
LENGTH: 3522
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APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING
FILE REFERENCE: PB-0014 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Incyte NAME/KEY: unsure LOCATION: 656, 658, 663 OTHER INFORMATION: a, t, c
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 1186 GAGGTCAACACCCAGGCCTACTGGAACTCCCTTGGAGAGAATAGAGACAGATATAAAAGCA 1245
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                              rHisGlyThrProGlnSerSerSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGl 197
                                                                  ACTGGAAAGCCAGGAAGTGCAGGAATCATTTCATCAGGGCCCAATAACTACACCACCCCT
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	Qy 504 euGluvalLeuvalGlyThrGlyThr	Qy 515 lualaLysLeuGlnGluPro	Oy 522TrpSerCysTyrMetCysLeuProGlnArgCysHisGlyValLeuArg 537	RESULT 6 US-09-041-886-18 US-09-041-886-18 Sequence 18, Application US/09041886 Sequence 18, Application US/09041886 Sequence 18, Application US/09041886 GENERAL INFORMATION: APPLICANT: Bredesen, Dale E. APPLICANT: Bredesen, Dale E. TITLE OF INVENTION: OCRESSONDENCE S. CORRESSONDENCE S. ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700 CITY: San Diego CITY: San Diego STATE: California COMNTR: Only Strem: Campbell & Flores LLD SOFTWARE: Perpoy disk COMNTR: APPLICATION DATA: COMNTR: APPLICATION DATA: APPLICATION UNMER: US/09/041,886 FILING DATE: CLASSTRICATION NUMBER: B- SOFTWARE: PROBELIN Release #1.0, Version #1.25 CHARSTATION NUMBER: PLOY 100: FILING DATE: FILING	Alignment Scores: 0.0144 Length: 4481 Score: 137.50 Matches: 108 Percent Similarity: 33.46\$ Conservative: 63 Best Local Similarity: 21.14\$ Mismatches: 211 Query Match: 4.01\$ Gaps: 18	US-09-720-086-8 (1-853) x US-09-041-886-18 (1-4481) Qy
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CTGTTACCCCTTCTAGTGAGGCTAAAGATT---
                            MetTyrHisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSerSerPro 321
                                                                                          LeuPheSerGlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLysAla 301
                                                                                                                                   GAAATACCCCCAGTGGGCCAGTTCTTGCTTCTCCCCAAGCTGGTATTATTCCAACTGAAG
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GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin an
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
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Best Local Similarity:
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                                                                                                                                                                                                                                                              US-09-720-086-8 (1-853) x US-09-105-537-5 (1-36778)
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                                                                                                                                                                                           31747 GGGCGTGTGGGGGTGGTGCCGCGGATGCG------CGGGGTGCGGCGCGCGTGGG
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TYPE: DNA
                                                      31642 GCCTCGGCGTCCAGG
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                   70
                                                                                                                                                                                                                          10 GlyGluGluAspAlaGlyGlyArgGluAspSerIleLeuValAsnGlyAlaCysSerAsp
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399 uLysThrAsnCysTyrAsnAsnGlyLysAspArgGlyAspGluAspGlnSerArgGluGl 419
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Sequence 19, Application US/09320878A
Sequence 19, Application US/09320878A
Sequence 19, Application US/09320878A
Sequence 19, Application US/09320878A
PRESENT 611659
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: McDANIEL, Robert
APPLICANT: TANG, Li,
TILE REPERRENCE: 30662200210
CURRENT TANG, Li,
TILE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30662200210
CURRENT APPLICANTON NUMBER: US/09/320, 878A
EARLIER PELLING DATE: 1999-06-27
EARLIER PELLING DATE: 1999-04-30
EARLIER FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 60/119, 139
EARLIER FILING DATE: 1999-04-30
EARLIER FILING DATE: 1999-05-20
EARLIER FILING DATE: 1999-05-20
EARLIER FILING DATE: 1999-05-20
EARLIER FILING DATE: 1999-05-22
EARLIER FILING DATE: 1999-05-28
SOUTHARE: PLENDING UNDER: 60/087, 080
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Matches:
Conservative: 4
Mismatches:
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LENGTH: 38506
TYPE: DNA
ORGANISM: Streptomyces venezuelae
)9-320-878-19
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ee: 137.50
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399 uLysThrAsnCysTyrAsnAsnGlyLysAspArgGlyAspGluAspGlnSerArgGluGl 419
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Best Local Similarity:
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                                                                                                                                 US-09-720-086-8 (1-853) x US-08-923-137-1 (1-35524)
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                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                 17568 TCAGTGGCGCTGCGAGGCCTGAACCGCCACGGAAGCTATGCCTGGTATCGCCCCGATCGC 17509
17508 CGCGGCTATGATGGGGATCAGAGCAGGCAGAAAGCCACCCCCAGCCTCTTGCTGATAGC 17449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28782 TCCGGGCCGGTGACGTCCAGCGGATCGCCGCCCGGTG
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APPLICANT:
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LENGTH: 35524 base pai
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NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,
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APPLICATION NUMBER: US 60/024,700
FILING DATE: 06-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                      No.:
                              122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
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                            ArgSerThrArgGlyArgGlnGlyArgAsnHisValAspGluSerProValGluPhePro
                                                                                             AlaValArgThrArgAsnAsnAsnSerValSerSerArgGluArgHisArgProSerPro
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                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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Krishna J.
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Matches:
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\$ g	371	IUSerArgLysTyrGluAsnLysThrArgArgArgThrAlaAspAspSerAlaThrSerA 391
ò	391	sp-TyrCysProAla 395
qq	16368	::: CTTTTTGTCCTTTTTGACCCGCTTGATTTTTGCGGGGCTTTTTTTCATCCTTCACGGGG 16309
ò	396	ProLysArgLeuLysThrAsn 403
qq	16308	GACCGTAGATTTCAGGCGCGCATGACCTGGAGCATCTCTTCCTTGTATTTGCGCTTGGACA 16249
ò	404	6
qq	16248	TCCTCGCTGGGACACAACATCGGA16225
à i	420	DValAlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSer 437
ĝ ;	16224	5
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ò	454	
q	16113	TGGCAATGGCCGCTGCTGCAGTGGCTGCGCGCCTGGGGGACCTGCCAGCACTGGCAC 16054
ò	463	LeuGlu
qq	16053	:: CTGAAGCCGCGCGTCTGGCTGCTCTAAGCATAGCTCTTCGCCCCACGCGTTTGGCTCTCC 15994
ò	465	LeuPheTyrMetTyrAspAspAspAspGlyTyrGlnSerTyrCygThr 479
qq	15993	GTAGCAAAGCTCTTGCTGCTCGCATAGCGGGGGGTGCCCGGTGGCGCTGGCGATGCGTC 15934
ò	480	ValCysCys
qq	15933	TCCGCCTGCTCTTCCGGCGAGCATAGGCGCGGGCGTCACTACTACGCTGTCAATAACTG 15874
ò	493	rSerCysCysArgCysPheCysValGluCysLeuGluValLeuValGly 509
đ	15873	CATCCACAGTAGATGTAGGAGTAGGAGTATAAGTTACGAGCATCGGCCACCACCTGGT 15814
ö	510	ThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSe 523
g	15813	CGATCACATCATCGACGGTGGTTCTAGTGCGGATACGGCCCTTGAGGGCGCCCCCATGGAG 15754
ò	523	rCysTyrMetCysLeuProGlnArgCysHisGlyValLeuArgArg538
q	15753	cacagaaardrecacacacacacadaaadrachararadaacarrracaagcac 15700
ò	539	ArglysAspTrpAsnValArgLeuGlnAla548
g	15699	CTCCGTACATCTTGCTTGGCGCGCGCAGGCCCCAACCGGTGTTATTACTAGGTG 15646
ò	549	
g	15645	AGATAAGAATGGACATTTTTTTTTTTTTAGAAAGTGCGGCTTGAAAGGACGCGCGCG
ò	295	SLeuTyrProAlaIleProAlaAlaArgArg 572
q	15585	
RES US: S	ULT 10 08-760 equenc atent APPL APPL APPL	e 4, Application US/08760745 No. 5972658 LINFORMATION: LICANT: Bandman, Olga LICANT: Goll, Surya K. LCANT: Murry, Lynn E.
	1	WENTEDN: EONG GROWIN FACIOR

NUMBER OF SEQUENCES:

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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ADDRESSEE: INCYTE PHARMACEUTICALS,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 598956
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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CITY: Palo Alto
STATE: CA
COUNTRY: US
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                                                                                                                                                                                                                                                                          146 LeuArgArgAlaThrAlaSerAlaGlyThr---ProTrpProSerProProSerSer 164
                           207 AlaAspSerGlyAspGlyAspSerSerGluTyrGlnAspGlyLysGluPheGlyIleGly 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2376 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                   GlnAspSerGln------GlnGlyGlyMetGluSerProGlnValGlu 206
                                                                                                                                                   AspThrGluAspThrHisGlyThrProGlnSerSerSerThrProTyrAlaArgLeuAla 192
                                                                                                                                                                                  GTGCGGCGCGGGGGGGAGACGCCGTGGCCGCGCCGGAGCTCGGGGCCGGGGGGCCACCATC 201
                                                                                                                                                                                                               ACTCGÁCGAGCGCGCACCCACCGCGCCGGAGCCTTGCCCCCGATCCGCCCCGCCCCGTCC 141
                                                                                                                                                                                                                                                                                                          GGGTGGAGGAGAGGCCTCGCGCAGAGGAGGAGCAATTGAATTT---CAAACACAAACA 81
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- TCGCGATCCAACCGGCAGAAGGAGTACAAATGCGGG
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Matches:
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Indels:
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SULT 11 10-036-987A-1/c 109-036-987A-1/c Sequence 1, Applicatio Patent No. 6143526 GENERAL INFORMATION: APPLICANT: Baltz, APPLICANT: Brought APPLICANT: Crawfor APPLICANT: Mexio, APPLICANT: Mexio, APPLICANT: Treadwa APPLICANT: Waldron TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES CORRESPONDENCE ADDR	452 yGlyLeuCysGlnThrC	438 sGlyArgLysAsnPro	420 MetAlaSerA: 988 ACCAAGGAAGJ	407 GlyLysAspA: 928 GGCTCTGGCCC	390 SerAspTyrCysPro ::: 868 TTGGAGGTTGAGAGGCCC	372 SerArgLysT) 808 TCTCCTAAACC	360748 GCCAAGGAGA	341 LysProThrGlyIleGl 688 AAGAAGGGGAATGCAGA	322 GlyAspSerLeuG 628 AAAAAGAGCTGTG	302 MetTyrHisAl :::::: 571 CTGTGGGAGAT	282 LeupheSerGlnHi ::: 517 GAATCCAAGGAGAA	262 GlnTrpPheGly ::: 457 TTTTTTTCGGG	244ValSe :: 415 CCTGAGGCTGC	227 AspLeuValTr :: 355 GACCTGGTGTT
n US/09036987A Richard H. on, Mary C. d, Kathryn P. Krishnamurthy Donald J. y, Patti J. Jan R. Clive Biosynthetic Production 39 ESS:	LeuCysGlnThrCysArg 459 ::: CTGGCCATGGCCTGCAAA 1120	ValSerPheHisP CACC	AlaSerAsp-ValAlaAsnAsnLysSerSerLeu 	BABPAT9G1yTGGCCGGGGGGGCCTCCCCAAGAGAGA	CysProAlaProLysArgLeuLy 	erArgLysTyrGluAsnLysThrArgArgArgThrAlaAspAspSerAl 	GerlysValargArgAlaGlySerArgLysLeuGlu 	Y11eGluGlyLeuLy8ProAsnAsnThrGl TGCAGAGGGCAGCAGCGAGGAAGGGAA	luAspGlnLeuLysI ::::: :::: TGGAAGAGCCTGAA	MetTyrHisAlaLeuGluLysAlaArgValArgAla ::: CTGTGGGAGATCGAGAACAACCCTACTGTCAAGGCT	heSerGlnHisPheAsnLeuAlaThrP ;;; CCAAGGAGAAGTTTGGCAAGCCC	YASDG1YLYSPheSerG1uVa1Se	rTrpLysAlaT ; ::: CGTGAAATCAA	pGlyLysIleLysG : ::: cGccaagaTGAAGG
Genes For Spinosyn		ro	GluAspGlyCy ATGAGAGCCTG	AspGluAspGlnS ::: ::: CCAAGAGGAAGAAGAAGAGGAGGATGAAG	sThrAsnCys ; AAAGAATAGC	gArgThrAlaAsp ;;; ,cccTgaaggagagaag	sValArgArgAlaGlySer. AAGAGGAGAGCAGGGGAC	uGlyLeuLy8ProAsnAsnThrGlnProValValAsnLy8 	ProMetleuGluTrpAlaHisG CAGAGCCCGAAGCTGCAGAGG	GlyL T	heAsnLysLeuValSer AACAAGAGGAAAGGG	rAlaAspLysLeu CCCCAAAGACCTC	hrSerLysArgGlnAlaMetSerGlyMe :: CAGCCAACAAATACCAA	SerTrpTrpProA CCACACTGGCCGG
Insecticide		-LeuPheGluG1 452 :::	SLeuSerCY 438	SerArgGluGln 419 GAGGAAGAGGCT 987	TyrAsnAsn 406 ::: ACCCCTCTGAGCCC 927	AspSerAlaThr 389 ::::: GAGGCAGCCACC 867	SerArgLysLeuGlu 371 ::: GACTTGCTGGAGGAC 807	nProValValAsnLys 359 : ::::::: GCTGGTCATTGATGAGCCA 747	aHisGlyGlyPhe 340 AGAGGGTGACGGTGAT 687	ysThrPheProSerSerPro 321 ::: ccggcTaTCAGTCCTCCCAG 627	TyrArgLysAla 301 ::: ::: TTCAGCGAGGGG 570	ValAlaLeuGly 281	MetArgTrpVal 261 GTC 456	laMetVal 243 ::: CCCGGATTGACGAGATG 414

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29836 ACCGTCCTGATTCACCGCACTACCACGAACAACCGCCAGCACCTCATGCCCATTCCGCCG 29777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29716 CGCACCCGCGCGAACGACTTGCACCGCCCATCCGGCGCGAGAGCCCCGTTGGCGGGAGAA 29657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29596 CTCACCGGCCCGCAGTGCTTGCCCCGCCAGGTGCAACGCCACCAACGACGACGAACACGC 29537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29476 AACCGCTGCCGCACCCGTCAGCACATGACCTGCCACCGCAGGCGGCGCGCGTCCGCAA 29417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29776 GGCATCCGACAACCGCTCCAGCAACAACAGTCCGGCACCCTCACCCCATCCAGTGCCATC 29717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 -----ValArgThrArgAsnAsnAsnSerValSerSerArgGluArgHisArgProSer 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ProArg-----SerThrArgGlyArgGlnGly 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 AlaileArgThrPro----Gluile 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 SerIleLeuValAsnGlyAlaCysSerAspGlnSerSerAspSerProProIleLeuGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 ArgGlyArgArgSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 ThrGlnAspLeuThrGlyAspGlyAspGlyGluAspGlyAspGlySerAspThrProVal 86
                                                  ADDRESSE: Dow AgroSciences LLC Patent Department STRET: 9330 Zionsville Road CITY: Indianapolis STATE: Indiana
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-720-086-8 (1-853) x US-09-036-987A-1 (1-80161)
                                                                                                                                                                                                                                                                                                                                                               LELEFANCE (317) 337-4847
TELEFAX: (317) 337-4847
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 80161 base pairs
TYPE: nucleic acid
STRANDEDNESS; double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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129.50
32.91%
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DB:
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MOLECULE TYPE:
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S &	29356	Argashtisva.Aspeiuserrrovalgiurhekro-Alainakrgserleuargar 148
1	0	TCCAGCAACCG 292
ò	148	gArgalaThrAlaSerAlaGly
g	29296	CTGCTGCGGATCCATCGCCAGCGCCTCACGCGGCGAAATCCCGGAAGAAACCCGCGTCGAA 29237
à	156	ThrProTrpProSerProBerSerTyrLeuThrIle 168
q	29236	CTCCGACACGCCTGAAGAAAACGCCCGCGCGGGATACGACGTGCCAGGACGATCGGA 29177
ò	169	-AspLeuThrAspAspThrGluAspThrHisGlyThrProGlnSerSe 184
đ	29176	GICCGGAACGAACACGCCAICCAGGTCCCATCCGCGATCCCCCGGAACTICGGAGATCGC 29117
ò	184	rSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMetGluSer 202
g	29116	
ò	203	ProGlnValGluAlaAspSerGlyAspGlyAspSerSerGluTyrGlnAsp 219
q	29062	GGGATAACGACAACTCATCGCCACGATCGCGATCGTCCTTCTCCGCGGAGAACCG 29003
ò	220	
пр	29002	ATCCCTGCCGCGCGGAGGCGTTCGTTCCCTTGAGCGATGCTCGCAGTGCCTCGACAAC 28943
ò	234	ysGlyPheSerTrpTrpProAlaMetValValSerTrpLysAlaThrSerLysArgGlnA 254
q	28942	TTCTTCGTAACTGGTGGTCACCGTCATCTCCCAGGTCGG 28904
ò	254	lametSerGlyMetArgTrpValGlnTrpPheGlyAsp-GlyLysPheSerGluValSer 273
g	28903	CGGTCTCAGGACTCGCGTTCGCCCAGCGCTGCTTCGACGAGGCCGGCTACATCCATC
ò	274	aAspLysLeuValAlaLeuGlyLeuPheSerGl
В	28843	rearceagereegecearcerecadeagaracegagreeacter 28790
ò	292	
q	28789	CCGGCAAGTGCGAGCAGCGGACTCACCAGCCTGCCTCGCGCAAGGCCGGGAACGGG 28733
ò	302	MetTyrHisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSer 319
g	28732	ATCGACGTCAGTGCCGCTTCGTGCGCCTCGTCCTCGGGAATGCCTGCTCTGCG 28673
ò	320	SerProGlyAspSerLeuGluAspGlnLeuLysProMetLeuGluTrpAlaHisGlyGly 339
q	28672	GACTCGGGAAGAAGCCTCGCC
ò	340	PheLysProThrGlyIleGluGlyLeuLysProAsnAsnThrGlnProVal 356
q	28639	GCCAGTTCCGCAGGCGTGGGATGGCTGAAGATAATTGTCGATGGCAACTGGAGGCCGGTA 28580
ò	357	ValAsniysSeriysValArgArgAlaGlySerArgLysLeuGluSerArgLysTyrGlu 376
g	28579	GCTCGATTGAGCCGAACGCGGAGTTCGACCGCGGCCTGCGAGTCGAATCCGCTGTCC 28523
δ	377	AsnLysThrArgArgArgThrAlaAspAspSerAlaThrSerAspTyrCysProAlaPro 396
qq	28522	-12:
ò	397	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QQ	28471	AGAGCGGTTTCGCCGCGTACCAGCTCCTGTTCCTGTGTCGGCCTCGGTGCC 28412
ò	408	LysAspArgGlyAspGluAspGlnSerArgGluGlnMetAlaSerAspVal 424
엄	28411	GCGGACAATCGCTGCCGCCATTCCAACGACGCGTCGGCAAGGACTCCCCGCCTCGGGCTGG 28352
ò	425	AlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArgLysAsnPro 443

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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Kathryn P
APPLICANT: Careford, Kathryn P
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Maldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIV1
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
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US-09-370-700-1/c
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
LENGTH: 80161
YPE: DNA
KGANISM: Saccharopolyspora spinosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09370700 Patent No. 6274350 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28351 GCATCGACGAGGAGTTCCTTGACCTCGGCCAGTTCGTTCAGCAGCGGCCGC-----
                                                                                                                                           29776 GGCATCCGACAACCGCTCCAGCAACAACAGTCCGGCACCCTCACCCCATCCAGTGCCATC 29717
                                                                   29716
                                                                                                                                                                                                                                29836 ACCGTCCTGATTCACCGCACTACCACGAACAACCGCCAGCACCTCATGCCCATTCCGCCG 29777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28150 CCTGTTTCTCCGGAGGCCATGCCCTCGCCGGCCCACGGC 28112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28246 ACCAGGGAAATTTCGTCCTGTTCC----ACGGCCTGCCGGATTCCGGCGATGGCGTGC 28193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28285 ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 CysTyrMet-----CysLeuProGlnArgCysHisGly 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 GlyArgGluLeuLeuLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCys 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 GluLeuPheTyrMetTyrAspAspAspGlyTyrGlnSerTyrCysThrValCysCysGlu 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444 ValSerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysArgAspArgPheLeu 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 -----
                                                                                                        47
67 ThrGlnAspLeuThrGlyAspGlyAspGlyGluAspGlyAspGlySerAspThrProVal 86
                                                                                                                                                                                    40 AlaileArgThrPro-----
                                                                                                                                                                                                                                                                   20 SerIleLeuValAsnGlyAlaCysSerAspGlnSerSerAspSerProProIleLeuGlu
                                                        CGCACCCGCCGAACGACTTGCACCGCCCATCCGGCGCGAGACCCCCGTTGGCGGGAGAA 29657
                                                                                                 ArgGlyArgArgSerSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TGCGGAGCCATTGGGGAAAGGCCGTATCGGCGCAGCTGGTCT 28151
                                                                                                                                                                                                                                                                                                                                                                         10.6
129.50
32.91%
21.57%
2.84%
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                                                                                                                                                                                      -----GluIle 46
                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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28	39 GCCAGTTCCGCAGGCGTGGGATGGCTGAAGATAATTGTCGATGGCA	당 .
al 356	lyIleGluGlyLeuLysProAsnAsnTh:	٥ و
22 1	2 GACTCGGGAAGAAGCCTCGCCCG	B 1
	320 SerbroglyBanderLendlinBandlaLieuTreMortenidlinTrnBladiaGlidl	ટ્
er 319 :: CG 28673	302MetTyrHisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSe ::: :::	당 성
GG 28733	28789 CCGGCAAGTGCGAGCAGCGGACTCACCAAGCCTGCCTCGCGCAAGGCCGGGAACGGG	망
301	292PheAsnLysLeuValSerTyrArgLysAla	δ
GT 28790	28843 TCGATCGAGGTCGCGCCGCATCGTCCGAGGAGATACCGGAGTCGACCGGGTGT	Дb
291	LeuPheSerGlnHisPheAsnLeuAlaThr	Q
, N 1		문 4
	CAACTGGTGGTCACCGTCATC	5 8
254		. Q
AC 28943	29002 ATCCCTGCCGCGCGGAGGCGTTCGTTCTCCTTGAGCGATGCTCGCAGTGCCTCGACAAC	Д
.еL 234	220GlyLysGluPheGlyIleGlyAsp-LeuValTrpGlyLysIle	8
CG 29003	29062 GGGATAACGACAACTCATCGCCACGATCGCGATGGGATCGTCCTTCTCCGCGGAGAACCG	문 4
) E
	184 rSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMetGluSer	5 5
:: GC 29117	29176 GTCCGGAACGACACCCATCCAGGTCCCATCCGCGATCCCCCGGAACCTTCGGAGATCGC	뭕
Se 184	169 -AspLeuThrAspAspThrGluAspThrHisGlyThrProGlnSers	Ş
N	w	밁
168	156ThrProTrpProSerProProSerSerTyrLeuThrIle	δ
N	29296 TGCTGCGGATCCATCGCCAGCGCCTCACGCGGCGAAATCCCCGAAGAAACCCGGCGTCGAA	뭥
155	148 gArgAlaThrAlaSerAlaGly	Ş
Ar 148 CG 29297	130 ArgAsnHisValAspGluSerProValGluPhePro-AlaThrArgSerLeuArgAr	유 성
GT 29357	29416 CCACGACGCGTAGTCCTGGCCATTGGTGCCGACGAACACGCCAACGCGGGAACCGCGTGT	дb
ly 129	121 ProArgSerThrArgGlyArgGlnGly	Ş
AA 29417	29476 AACCGCTGCCGCACCGCCCGTCAGCACATGACCTGCCACCGCAGGCGGCGGCGTCCGCAA	ДD
er 120	103ValArgThrArgAsnAsnAsnSerValSerSerArgGluArgHisArgProSo	γQ
AG 29477	89 LysLeuPheArgGluThrArgThrArgSerGluSerProAla :::::	영 2
GC 29537	29596 CTCACCGGCCGCAGTGCTTGCCCCGCCAGGTGCAACGCCAACGACGACGACGAACACGC	밁
88	87 MetPro	γ
CA 29597	29656 CTCCAGGAACACCTTCGGCGTCGACATCACCGTGACGCCACCGGCAAGGGCCAAGGTCGCA	рb

US-09-720-086-8 (1-853) x US-09-491-772-1 (1-8580) Qy 85 ProValMetProLysLeuPheArgGluThrArgThrArgSerGluSerProAlaValArg 104	5708 CCTATTACACCCAGGCGCTGTTTGCCCAGGACCAGATCGACATCGCCCGCGCCAGA 105 Thrardaenasnasnasnasnasnasnasnasnasnasnasnasnasn	5765 AGAAGGCCTTCGAACAGTTCCAGCAGACAGCGCACCTGTTCGAGCAGGGCGAGGCA	Oy 119 ProSerProArgSer 123	Oy 124 Thrarg-GlyArgGlnGlyArgAsnHisValAspGluSerProValGluPheProAlaTh 143	Qy 163 rSerTyrLeuThr-1leAspLeuThrAspAspThrGluAspThrHisG 179	Qy 179 ly-ThrProGlnSerSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGly 198	199 Gly	Qy 211 AspGlyAspSerSerGluTyrGlnAspGlyLysGluPheGly1leGlyAspLeuValTrp 230	Qy 231 GlyLyslleLysGlyPheSerTrpTrpProAlaMetValValSerTrpLysAlaThrSer 250	Oy 251 LysargdlnalaMetSerGlyMetargTrpValGlnTrpPheGlyaspGlyLysPheSer 270	Qy 271 Glu271	Oy 272ValSerAlaAspLysLeuValAla	Qy 280LeuGly	Qy 285 GlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLysAlaMet 302	Qy 303 TyrHisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSerSerProGly 322	Qy 323 AgpSerLeuGluAspGlnLeuLysProMetLeuGluTrpAlaHisGlyGlyPheLysPro 342	Qy 343 ThrGlylleGluGlyLeuLyBProAsnAsnThrGlnProValValAsnLy8SerLysVal 362
Qy 357 ValAsniysSerLysValArgArgAlaGlySerArgLysLeuGluSerArgLysTyrGlu 376	Db 28579 GCTCGATTGAGCCGAACGCGGAGTTCGACCGCGGCCTGCGAGTCGATCCGCTGTCC 28523 Qy 377 AsnLysThrArgargArgThrAlaAspAspSerAlaThrSerAspTyrCysProAlaPro 396	Db 28522 TTGAAGGCTCGTTCCGATGCAACGCCGCTGCCCCGGGGTGTCCCAGCACC 28472 Ov 397 LV8	28471 AGAGCGGTTTCGCCGCGTACCAGCTCCAGGATCAGCTGTTCCTGTGTCGGCCTCGGTGCC		444 ValSerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysArgAspArgPheLeu 28300	<pre>Qy 464 GluLeuPheTyrMetTyrAspAspAspAspAlyTyrGlnSerTyrCysThrValCysCysGlu 483</pre>		Oy 504 LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSer 523 Db 28192TGCGGAGCCATTGGGAAAGGCCGTATCGGCGCAGCTGGTCT 28151	<pre>Qy 524 CysTyrMetCysLeuProGlnArgCysHisGly 534 bb 28150 CCTGTTTCTCCGGAGGCCATGCCTCGCGGGCCCACGGC 28112</pre>	шo	; GENERAL INFORMATION: ; APPLICANT: Rhee, Joon Shick ; APPLICANT: Pan, Jae Gu ; APPLICANT: Ahn, Jung Hoon	APPLICANT: Korea Advanced Institute of Science and Technology(KAIST) ; TITLE OF INVENTION: ARC Transporter Gene Cluster in Pseudomonas fluorescens for ; TITLE OF INVENTION: Enhanced Lipase Secretion ; FILE REFERENCE: 0136/00650		SEQ ID NOS: KOPATIN 580	; TYPE: DNA ; ORGANISM: Pseudomonas fluorescens US-09-491-772-1	Alignment Scores: 0.535 Length: 8580 Pred. No.: 126.00 Marches: 104 Percent Similarity: 34.84\$ Conservative: 42	: 24.82% Mismacches: 2.76% Indels: 4 Gaps:

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           US-09-720-086-8 (1-853) x US-09-179-558-54 (1-2874)
                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                         TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                       NAME: COruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S.
FILING DATE: 15-APR-1998
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Muchuswami, Rohini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TARGETING DNA METABOLIC PROCESSES USING
TITLE OF INVENTION: AMINOGLYCOSIDE DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nuence 54, Application US/09179558
ent No. 6180612
ERAL INFORMATION:
HPPLICANT: Hockensmith, Joel W.
                                                                                                                                                   TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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CTTY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CO
OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 27-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-911-853-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13146 CCCCTGGGGCAACCAGTACCTGTACCTGTCGCCGGGCACCCGGGCAAGATCGACCTGTA 13205
                                                                                                                                                                                                                                                             13452 GGCGGTGCTGGACAACCGCGAGTATGGCGTACGCTTCGACGCCCGGAGCTACCGGGTGCT 13511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13206 TTCGCTGGGCGCCGACGGCCA-----GGAAGGCGGCGACGGGACCGACGCCGACAT 13256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13578
                                                                                                                                                                                                                                                                                                                                                                                             13416 -----GCGCCTGCAGTCGCTGCTGCTGCTGCTGCTGCTCGACGA 13451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13317 GCTGGTGGTGCTGGTGCTGGG------ 13340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13548 CGACGAGCGCGTGCACGAGCTGCC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 359 | CETECTCEGCAGCEGGATCGCCAGCAGCCCCGCGCAAGCTGGCGGACGAGCCCGA--- 13415
                                                                                                                                                                                                                                                                                                                                                             152 AlaSerAlaGlyThrPro-----Trp------ProSerProProSerSer 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 SerSerArgGluArgHisArgProSerProArgSerThrArgGlyArgGlnGlyArgAsn 131
                  224 GlyIleGlyAspLeuValTrp-----GlyLysIleLysGlyPheSerTrpTrpProAla 241
                                                                                                                                                      205 ValGluAlaAspSerGlyAsp---GlyAspSerSerGluTyrGlnAspGlyLysGluPhe 223
                                                                                                                                                                                                                                                                                             165 TyrLeuThrIleAspLeuThrAspAspThrGluAspThrHisGlyThrProGlnSerSer 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  720-086-8 (1-853) x US-08-911-853-29 (1-17612)
                                                                                                                                                                                                                                                                                                                                                                                                                            132 HisValAspGluSerProValGluPheProAlaThrArgSerLeuArgArgArgAlaThr 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ArgGluValSerSerLeu-------LeuSerTyrThrGlnAspLeuThr 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 LeuGluAlaIleArgThrProGluIleArgGlyArgArgSerSerSerArgLeuSerLys 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 ArgGluThrArgThrArgSerGluSerProAlaValArgThrArgAsnAsnAsnSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 GlyAspGlyAspGlyGluAspGlyAspGlySerAspThrProValMetProLysLeuPhe 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 GluAspSerIleLeuValAsnGlyAlaCysSerAspGlnSerSerAspSerProProIle 37
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 ArgHisLeuAsnGlyGlu-------GluAspAlaGlyGlyArg
                                                                                                                            -----GCTCGAGCTGGAGATCGAGGTCGACGAGCAGAGTGTCGGGGCTGCCCGCCGC--- 13628
                                                                                                                                                                                                                              SerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMetGluSerProGln 204
                                                               -----CCGTGGCGAGCAGGACAAAGCCGCGGCCAAGGCCGCCACAGCTGCT 13673
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ArgValle 578 CTGGCAGC 14549	7 eProAlaAlaArgArgArgProIle	1449	유 왕
CG 14	3CTGGCGCA	1447	DЬ
aIl 567	7 nAlaPhePheThrSerAspThrGlyLeuGluTyrGluAlaPro	547	; 15
ArgLeuG1 547	sLeuProGInArgCysHisGlyValLeuArgArgArgLysAspTrpAsnVal ::: CCGCGACACCCAGCTGGAGTTCACCCGCAGCGG	14440	9d 6
, ,	GCGACCCGCTGGGCGACCTGCCAGCCAGCAGCAGTGG	1439	, D
TyrMetCy 527	Val-GlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSerCys	ர	; 15
14393		1434	뫄
/alLeu 507	.88 LeuLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCysLeuGluV	4 8	γQ
	07GCCAGCAGGAGCAGCTCTGCGCGAGCTGACGCCGACCCA	1430	당 4
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r 467	0 PheGluGlyGlyLeuCyeGlnThrCysArgAspArgPheLeuGluLeuPheTy	450	} &
RGCCA 14255		14196	Дb
ProLeu 449		430	δ
::: GAGGC- 14195		1413	Db
ysser 429		415	Ş
CTGCAGGGCA 14136	TCACCGTACGGGTGGCGCTGCGGCCGGAGCGCGGG	14092	d d
3luAsp 414	ProLysArgLeuLysThrAsnCysTyrAsnAsnGlyLysAspArgGlyAs	ω	Ş
CGTG 1	4	1405	Db S
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-	CTGGCGGACAACCGCCTGCAGGAGCT	13947	당 .
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ACCTGG 13946	Introduction	13908	B 2
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315)6 ValSerTyrArgLysAlaMetTyrHisAlaLeuGluLysAlaArgValArgAlaGlyLys 	296	Ş
13862		13836	D
LysLeu 295	77LeuValAlaLeuGlyLeuPheSerGlnHisFheAsnLeuAlaThrPheAsnLys	277	Ş
TGCTCGAG 13835		1377	마
276		270	δ
::: CGCCGA 13775	CGGCGCGCGGTGCTGACGCTGGCCACGACGGCTT	13734	Db
LysPhe 269		256	γQ

Search completed: November 25, 2002, 03:06:35 Job time : 473.863 secs

Mon Nov 25 08:18:41 2002

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RESULT 1
US-09-276-531-47
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Sequence 47, Application US/09276531

Patent No. 6183968

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Hillmar, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Guegler, Jennifer L.

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

NUMBER OF SEQUENCES: 134
          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOPTWARE: Word Perfect 6.2 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION DATA:
APPLICATION UMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PH
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                  STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                 ZIP: 94304
                                                                                                                                                                                                                                                                                  STREET: 3174 POI
CITY: PALO ALTO
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US-08-474-933-1
US-09-307-621-1
US-09-179-558-61
US-09-179-558-61
US-09-179-236-7
US-09-147-236-7
US-09-147-236-1
US-09-103-840A-1
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US-09-627-216A-9
US-09-624-693A-18
US-08-403-852D-1
US-08-510-646B-1
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US-09-320-878-19
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US-09-105-537-30
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Patent No. 5248670
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Sequence 31, Appl
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Sequence 5, Appli
Sequence 19, Appli
Sequence 19, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 1, Appli
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61, Appli
1, Appli
7, Appli
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LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTTUT02
CLONE: 1271435
US-09-276-531-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TPLEPRONE (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       648 GlySerProCysAsnAspLeuSerAsnValAsnProAlaArgLysGlyLeuTyrGluGly
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                                                           537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspAspArgProPhePheTrpMetPheGluAsnValValAlaMetLysValGlyAspLys 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGG---CGGCTCTTCTTCGAATTTTC-CACCTGCTGAATTACTCACGCCCCAAGGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrGlyArgLeuphePheGluPheTyrHisLeuLeuAsnTyrSerArgProLysGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGGCNANTGCAACGATCTNNA-AATGTGAATCA-GCCAGGAAAGGCTGTATGAGGGAC
                                                                                                                                      IlePheGlyPheProValHisTyrThrAspValSerAsnMetGlyArgGlyAlaArgGln 827
                                                                                                                                                                                                                                                                                                                         AlaSerLysAsnAspLysLeuGluLeuGlnAspCysLeuGluTyrAsnArgIleAlaLys 767
                                                                                                                                                                                                                                                                                                                                                                                    AlaAlaHisAxgAlaAxgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProValIle
                                                                                                                                                                                                                                                                                                                                                                                                                               GATGACCGGNCGTTCTTCTGGATGTTTGAGAATGTTGTAGNCTCGTGCCGATTCGGCAGA
              AspTyrPheAlaCysGlu
                                                                           LysLeuLeuGlyArgSerTrpSerValProValIleArgHisLeuPheAlaProLeuLys 847
                                                                                                                                                                                                 LeuPheProValValMetAsnGlyLysGluAspValLeuTrpCysThrGluLeuGluArg
                                                                                                                                                                                                                                            TTAAAGAAAGTACAGACAATAACCACCAAGTCGAACTCGATCAAACAGGGGAAAAAACAA
                                                                                                                                                                                                                                                           LeuLysLysValGlnThrIleThrThrLysSerAsnSerIleLysGlnGlyLysAsnGln
                                                                                                                                                                                                                                                                                                      GCATCAAAGAATGATAAACTCGNGCTGCAGGACTGCTTGGAATACAATAGGATAGCCAAG
                                                           AAGCTGCTGGGAAGGTCCTGGAGCGTGCCTGTCATCCGACACCTCTTCGCCCCCTCTGAAG
                                                                                                                    NTCTTTGGCTTTCCTGTGCACTACACAGACGTGTCCAACATGGGCCGTGGTGCCCGCCAG
                                                                                                                                                                                 CTTTTCCCTGTTGTCATGAATGGCAAAGAAGATGTTTNGTGGTGCACTGAGCTCGAAAGG
                                                                                                                                                                                                                                                                                                                                                                   GCTGCTCACAGGGCCCGATACTTCTGGGGCAACCTACCCGGGATGAACAGGCCCGTGATA
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Matches:
Conservative:
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RESULT 2 US-08-913-832A-1

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPT0_spool/US09720086/runat_18112002_092957_29457/app_query.fasta_1.4252
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=65 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM=ext -HARPSIZE=500 -MAINLEN=0 -MAXD000000000
-USER=US09720086_@CGN_1_1_108 @runat 18112002_092957_29457 -NCPU=6 -ICPU=3
-NO XLPXY -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum
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                                                                                                                                                                                                                         Score
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                                                                                                                                                                                                                                                                                                                is derived by analysis of the total score distribution.
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Ygapop 10.0 , x
Fgapop 6.0 , F
Delop 6.0 , I
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                US-09-276-531-47

US-09-105-537-1

US-08-404-227C-1

US-08-458-568A-11

US-08-629-939-1

US-08-629-939-1

US-08-759-873-1

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equence 1,	Sequence 4, Appli	equence 12	equence 12	equence 19,	equence 5,	equence 30,	equence 72,	Sequence 76, Appl	equence 64,	equence 68,	equence 70,	equence 74, App	equence 1,	equence 66, App	e 7, Appl	equence 22,	equence 2,	equence 3, Appl	equence 3,	equence 93, App	equence 93, App	equence 1,	equence 1,	a Ce	equence 5,	equence 5,	e 22, App	equence 22,	equence 22, App	quenc	equence 23,	-

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ALIGNMENTS

US-09-276-531-47

Patent No. Sequence 47,

7, Application US/09276531 6183968

GENERAL INFORMATION:

Olga Jennifer

APPLICANT: APPLICANT:

APPLICANT:

Reddy, Hillman, Lal, Preeti Bandman,

Henry Roopa

ŗ

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 31
                                                                                                         APPLICATION NUMBER: U
                                APPLICATION NUMBER: 60/079, FILING DATE: March 27, 1998
                                                                                          CLASSIFICATION:
                   CLASSIFICATION:
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CALIFORNIA
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3174 PORTER DRIVE
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867 ValpheGlypheProValHisTyrThrAspValSerAsnMetSerArgLeuAlaArgGln 886
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                                                                                                                                                                                                                                                                                                                                  707 GlyserProCysAsnAspLeuSerlleValAsnProAlaArgLysGlyLeuTyrGluGly 726
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                                                                                                                                                                                                                                                                                                                                                         3 GGCGGCNANTGCAACGATCTNNAAAT-GTGAATCA-GCCAGGAAAGGCTGTATGAGGGAC 60
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REPRENCE/DOCKET NUMBER: 42,918
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 865-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS: LENGTH: 2077 base pairs
TYRE: nucleic acid
STRANDEDNESS: single
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748.00
81.95%
73.66%
15.16%
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                                                                                                                                                             LIBRARY: TESTTUT02
CLONE: 1271435
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IMMEDIATE SOURCE:
LIBRARY: TESTTUTO
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Best Local Similarity:
Query Match:
DB:
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US-09-105-537-1/c
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10619 CGGAGATCACCACCGGGGGCCGTTCA-----CGCGGGGCGACGCAGGCGGT 10569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 GlyGlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLeuProGluAlaSer---- 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 proAlaGluAla-----GlyLys-GluGlnLys-------GluThrAs 157
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Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, Y.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REPERENCE: 600, 438US1
CURRENT APPLICANT: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FREUESQ for Windows Version 3.0
SOFTWARE: FREUESQ for Windows Version 3.0
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                    TYPE: DNA; ORGANISM: Streptomyces venezuelae
US-09-105-537-1
                                                                                                                                                                                                                                                                                                                                                                                              Score: NO.: 0.00274
Score: 182.50
Percent Similarity: 3.84$
Best Local Similarity: 22.39$
Query Match: 3.70$
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Pred. No.:
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463 GluLysProLysValLysGluIleIleAspGluArgThrArgGluArgLeu---ValTyr 481
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                                                 GCAGCGCCCGTACCGCCAGATGCAGCGCCACCAGCGAGGAGGAGGAGCAGGCCGTCT-----
                                                                                                AlaAlaTyrAlaProPro--
                                                                                                                                                                                                GluGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGluAla 445
                                                                                                                                                                                                                                                  GGCCGTCGGCGGCCAGCCCCTTCTGCCGGGAGAACTCCACGAACGCCGCCGGATCGGCCA 9109
                                                                                                                                                                                                                                                                                                                                                  GCACGCCGACGCCCTCGGCCCAGCCGGTGCCGTCGGCGGCGGCCGAGAACGCCTTGCAGC 9165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGGCCGTTGGGCGCGGTCAGCCCGTTGGAGGCACCGTCCTGGTTGACCGCGGTGCCGG 9289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rgIleValSerTrpTrp------MetThrGlyArgSerArgAlaAlaGluGlyThrA 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GACAGCCCGGCGTCGGCGAGCGCCTCGGCGATGACGCGTTGCTGGG-----
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                                                                                             ---ProProAlaLysLysProArgLysSerThrAla 462
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US-09-720-086-7 (1-912) x US-08-804-227C-1 (1-43280)

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            Query Match:
                          Percent Similarity:
Best Local Similarity:
                                                     score:
                                                                             Alignment Scores:
                                                                                                        US-08-804-227C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08804227C Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 43280 hacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCI(DOS) TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8951 TCACCGCGTCGGCGCTGCCGGTCAGCAGAT 8922
                                                                                                                                               FEATURE:
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                              FEATURE
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                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                  No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: THOMAS G. PLA
STREET: LILLY CORPORATE
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CONTOPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 43280 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08, FILING DATE: February 21,
                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                     LOCATION:
                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LICANT: Kubstoss, Stuart A.
PUICANT: Rosteck, Paul R., Jr.
PUICANT: Sutton, Kimberly L.
FILE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----CCACCGTCATGGACGGTCCTTCGAGACCGAGCGCGTAGGAGATGCGGCCGGACA 8952
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20010.
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816.
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14351..19945
                                                                                                                     36249..41774
                                                                                                                                                                                                                                                                                                                      DNA (genomic)
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            0.011
182.50
32.84%
22.39%
3.70%
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                                                                                                                                                                                                                                                                                                                                                                                                                                             X-8231
             Length:
Matches:
Conservative:
Mismatches:
Indels:
43280
137
64
209
202
33
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à 8	2y 38 ArgGlnGluProSerThrThrAlaArgLysValGlyArgProGlyArgLysHis	Arglysarglyshis 57 ::: ::: scGACGCAGACGCGT 38431	
è 6	Oy 58 ProProValGluSerGlyAврThrProLysAspProAlaVallleSerLys	AlaValIleSerLys 74 ::: :GCACGG 38380	
දු ද	Oy 75 SerProSerMetalaGlnAspSerGlyAlaSerGluLeuLeuProAsnGly	ProAsnGly 91 CGGCGGCCACCAGCG 38320	
አ ብ	2y 92 AspLeuGluLysArgSerGluProGlnProGluGlyGerProAlaGlyGlyGlnLys :::	AlaGlyGlyGlnLys 111 ::: CCAGTTCGCCCA 38263	
දු ද	2y 112 GlyGlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLeuProGluAlaSer Db 38262 CCGAGTGCCCAGCAGCAGCATCCCCCAGTGCTCCAGCAGCGGGGGG	oGlualaser 129 GCAGCCGGTGGAGCG 38203	
ጵ ል	2y 130ArgalaValGluAsnGlyCysCysThrProLysGluGlyArgGlyAla	GluglyArgGlyAla 145 TCCGGTCCAGGAGTG 38149	
≿ 8	38148	GluThras 157 GCCCGCCGAGCAGCG 38089	
ጵ გ	2y 157 nIleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeu	uArgGlyGlyLeu 174 ::: sTATGGGGGATGCA 38029	
<u>ج</u> ۾	2y 175GlyTrpGluSerSerLeuArgGlnArgPro	GGAAGGCCATCCTGC 37969	
አ გ	2y 185MetProArgLeuThrPheGlnAlaGlyAspProTyrTyrIleSerL 	roTyrTyrIleSerL 200 	
हे ह	200 ysArg	laArgTrpLysArgG 213 CGCGGTGG 37856	
≿ 8	213	lugluAsnGlnGlyP 233 ::: CACGCGGGGCCC 37801	
ጵ გ	233 roGlyGluSerGlnLysValGluGlu	Alas 243 ::: :GCAGGCCGGCTCGT 37741	
સે લ	243 erProProAlaValGlnGlnProThrAspProAlaSerProThrValAlaThrThrPro- 	alAlaThrThrPro- 262 CGCCCCGGAGCCGC 37681	
ጵ ጵ	263GluprovalGlySerAspAlaGlyAspLysAspLysAspLytaglyThr	hr 275 :: cTTCGAGGACGACAT 37621	
⋩	276	277	
ą	37620	GGGGCCGGCCGGTCC 37561	
≳ 8	278GlyaspaspGlu378	-ProGluTyrGluAspGlyArgG 289 ::: GCCGGAGCTCCAGTCGG 37507	
≿ ક	289	erTrpTrpProGlyA 309 	

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APPLICANT: Schaffer, Priscilla A. APPLICANT: Why. Lily APPLICANT: Why. Lily TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus IIILE OF INVENTION: Infections
                                                                                                                                      37401 GCCCGATGTTGGACTTCAGCGAGCCGAGCGGGTGGTGGTCGCCGGAACGGTTCCGTC 37342
                                                                                                                                                                                                                                  37341 CGGAGGGGGCGAGCAGCGCCCCGGCCTCGATGGGGTCGCCGAGCCGGGTGCCGGTG---- 37286
                                                                                                                                                                                                                                                                                                                                   37206 CTGGGCCGTTGGGCGCGGTCAGCCCGTTGGAGGCACCGTCGTTGACCGCGGTGCCGG 37147
                                          37455 ĠĊ-----ÀĠĊĠĊĊTĠĠAGCATCTTGĂTĠĀĊĠĊĊĠĊĊĠACCGĠĊĠĠĊĠĠĊĠĠĊŢĠĠĊŦŢ
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                                                                                                 326 rgTrpValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetP 346
                                                                                                                                                                                            346 roleuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrA 366
                                                                                                                                                                                                                                                                                              366 rgLysAlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 MetileGluTrpAlaLeuGly------412
309 rglleValSerTrpTrp------MetThrGlyArgSerArgAlaAlaGluGlyThrA 326
                                                                                                                                                                                                                                                                                                                                                                                               386 alCysHisAspSerAspGluSerAspThrAlaLysAlaVal-GluValGlnAsnLysPro 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 -----GlyPheGlnProSerGlyProLysGlyLeuGluPro------ 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               446 AlaalaTyralaProPro-----ProProAlaLysLysProArgLysSerThrAla 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 GluLysProLysValLysGluIleIleAspGluArgThrArgGluArgLeu---ValTyr 481
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NUMBER OF SEQUENCES: 15

CAPRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
STRRET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 36813 TCACCGCGTCGGCGCTGAGCAGAT 36784
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Sequence 11, Application US/08458568A
Patent No. 5821339
GENERAL INFORMATION:
APPLICANT: Sch.f.
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity:
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NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFCI-0029
TELEFOROME: (215) 568-3100
TELEFOROME: (215) 568-3100
TELEFOROME: (215) 568-3149
TELEFOROME: (215) 568-3439
TELEFOROME: 1201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Herpes Simplex virus
STRAND: Herpes Simplex virus
TRANISM: Herpes Simplex virus
TRANISM: Herpes Simplex virus
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILLING DATE: 05-MAY-1993
CLASSIFICATION: 435
                                            6290
                                                                                                                                                                                                        6189
                                                                                                                                                                                                                                                                                                                                                                                                                                                 6021 TCGTCCGGACGCCTCCTCTACCATGGAGGCCAGCAGAGCCAGCTGTCGCGGCGAGACACG 6080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 02-JUNE-1995
                                                                                                                                                                                                                                                                                   6129 CGTCCCGCCGGGCGTCGTCGAGGTCGTGGGGGGTCGTGGTCGGGGTCGTCGTCCC 6188
                                                                                                                                                                                                                                                                                                                                                                 6081 CGTCCCCGGCGTCCTCGCCGGCGTCGGTGCCCGCCG------CGGGGGGCCCTCC 6128
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                                                                                                                                                                  107
138 ThrProLysGluGlyArg-GlyAlaProAlaGluAla-----GlyLysGluGlnLysGl 155
                                                                                                                                                                                                                                                                                                                                                                                                   48 ValGlyArgProGlyArgLysArgLysHisProProValGluSerGlyAspThrProLys 67
                                                                                                                                                                                                                                         88 LeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGluGlySerPro--- 106
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 -----LysAspGlyGluGluGluGluProArgGlyLysGluGluArg 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 Gln----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ProSerSerGlyProGlyAspThrSerSerSerAlaAlaGluArgGluGluAspArg---
                                                                                                                                                       -----AlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyAla-----
                                                                                                                                                                                                                                                                                                                         AspProAlaValIleSerLysSerProSerMetAlaGlnAspSerGlyAlaSerGluLeu 87
                                        CGCTGCTTGTTCTCCGACGCCATCGCCGATGCGGGGCCGATCCTCCGGGGATACGGCTGCG 6349
                                                                                                                        CGTCGCGGTCTGGGCTCGGG-GTGGGCCGGCGGTCGGTGGGGCCCGGGGAGCCGGGG 6289
                                                                                                                                                                                                        CGCCCT-----
                                                                             --AlaGluThrLeuProGluAlaSerArgAlaValGluAsnGlyCysCys 137
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172.50
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                                                                                                                                                                                                      ------CCTCCGTCTCCGCGCCCCACCCGAGGGCCCCCCCCT 6230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GluProSerThrThrAlaArgLy8 47
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Matches:
Conservative:
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458 rgLysSerThrAlaGluLysProLysValLysGluIleIleAspGluArgThrArg 476	Q
7057GCGGCCCAAGGGCCCCACCCTTGCCGCCCCCATTGGCCGG 7099	Db
440 rpValGluProGluAlaAlaAlaTyrAlaProProProProAlaLysLysProA 458	Qy
7025 CCCGCCGGACGCCAACGGGACCGGCGG7056	рb
420 ysGlyLeuGluProProGluGluLysAsnProTyrLysGluValTyrThrAspMetT 440	Qy
cccccccggrcc	Db
400 luValGlnAsnLysProMetIleGluTrpAlaLeuGlyGlyPheGlnProSerGlyProL 420	γQ
6944 CGGGCCCCGACTTCCCGGTTCGGCGGTAATGAGATACGAGC	ф
380 aGlyLysLeu-PheProValCysHisAspSerAspGluSerAspThrAlaLysAlaValG 400	Q
6926 CGGGCAGGGGGCGGGGCC 6943	рb
360 nLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGlnValAlaSerSerArgAl 380	Qy
6882CCGATCCGGCGGTTTCCGCTTCCGTTCCGCATGCTAACGAGGAA 6925	DЪ
340 sValGluLysLeuMetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAs 360	S
6863 CATGGCATCTCATTACCGC6881	DЪ
320 gAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLysPheSerValValCy 340	Q
6822TeagcagagacacGAGGGCGGTGGGTCCGCGCCCCCCCG 6862	дb
300 uArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMetThrGlyArgSerAr 320	9
6807 CCGCGCCATCTGCCA 6821	g
280 pGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLe 300	99
6767 GTGGCCGGGCCCGTTGGTCGAACCCCCGGCCCGAT 6806	дb
262ProGluProValGlySerAspAlaGlyAspLysAsnAlaThrLysAlaGlyAspAs 280	8
6707 CACCCCGAACGGAATTCCATTATGCACGACCCCCCCCCC	ф
256 oThr	8
6006600	В
236 rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr 256	Q
6629 TCGGGCTCATATAGTC	DЪ
216 sLysalaLysVallleAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSe 236	Q,
	Дb
208 aḥrgTrpTrpLysḥrgGluAlaGluLy 216	Q
6516CGCGTATCGGCGTCCCGGCGCGGCGGCGTCTGACGGTCTGTCT	DЪ
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175 yTrpGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAs 194	Q
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3025 CCAGGCGAGGGCACCCAGAGAACCCTGAGCCCAAAGAGCAGAGAGGCCTGGTTGAGGGA 3084
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                                                               2749 CTGGAAGAG---GAAGAGAACCTGGGAAAGGGAGGTACCAAGAG-----TCACTG 2796
                                                                                                                                                                                                     2797 AGGICTCTGGAGGAGGAGGACAGGAGCTGCCG------CAGTCTGCAGATGTG 2844
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26 GlyglugluglugluProArgGlyLysGlugluArgGlnGluProSerThrThrAla 45
                                                                                                                                      46 ArglysValGlyArgProGlyArglysArgLysHisProProValGluSerGlyAspThr 65
                                                                                                                                                                                                                                                                        66 ProLysAspProAlaValIleSerLysSerProSerMetAlaGlnAspSer---- 82
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7100 CGGCGGGACCGCCCCAAGGGGGCGGGGCCGCCGGGTAAAAGAAGAGGAACGCGAAAGCG 7159
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                                                                                                              1160 TTCGCACTTCGTCCCAATATATATATTAGGGCGAAGTGCGAGCAC 7209
                                                               477 ------GluArgLeuValTyrGluValArgGlnLysCysArgAsn 489
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MCKAY, Ronald D.G.
APPLICANT: Lendahl, Urban
TITLE OF INVENTION: Nestin Expression As An Indicator of
TITLE OF INVENTION: Neuroepithelial Tumors
NUMBER OF SECUENCES:
CORRESPONDENCE ADDRESS:
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Two Militia Drive
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ZIP: 02173

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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4641AAAA
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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APPLICATION NUMBER: US 07/660,412
FILING DATE: 22-FBB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,803
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; Sequence 3, Application US/07853913
; Patent No. 5338839
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08629939
Patent No. 5645995
GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESSEE: SUCHRUE, MION,
STREET: 2100 Pennsylvania
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RISK OF
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Best Local Similarity:
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DB:
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MOLECULE TYPE:
HYPOTHETICAL:
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REFERENCE/DOCKET NUMBER: A-
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CLASSIFICATION:
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                                                                                                                                                                                                            IleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu 177
                        AlaLysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSerGln
                                                             --- AGTCCCCCAGAAAAGGACAGCGGACTG-
                                                                                        IleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLys
                                                                                                                                                   SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyr 197
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	ProThrAppProAlaSerProThrValAlaThrThrProGluProValGlySerAspAla CCCGAACTTCCCGAAGATCCACCGCTGCCCCCCGCGGGGGTTTGTCCCCGCTC GlyAppLyBABANALAThrLyRAlaGlyAppBapGluProGluTyrGluAspGlyArgGly ATGAGCCGGTCCGGGTGCAAGGTTGGAAGACTCC
	cccGAACTTCCCGAAGATCCACCGCTCCCCCCCCCCCCCC
	GlyAspLysAsnalaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGly :::::
	ATGAGCCGGTCCGGGTGGAAGGTTGGAGACCAGCTC
	PheGly1leGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPrpro
	GlyhrgilevalSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp GCCGGG CCGGG ValMetTrpPheGlyAspGlyLy8PheSerValValCy8ValGluLy8LeuMetProLeu
	CCCCGG
	ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeu
	SerSerPheCysSerAlaPheHiaGlnAlaThrTyrAsnLysGlnProMetTyrArgLys
	SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys
	AlalleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCysGl
	CTGCCGTGCAGGTTGAGGAG
	HisAspSerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLysProMetIle
	GAGGATGGCTCTGAGTCCGAGGAGTCTGCGGGTCCGCTTCTGAAGGGCAAACCTCGG
Db 845	
Oy 408	8 GlutrpAlaLeuGlyGlyPheGlnProSerGly
Oy 422	,
Db 956	GCAGCAGGAGGCGTCGC
Qy 436	6 TyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProProAlaLys 455
Db 1016	6GCCCTGGTGGAGCAGGACGCGCCGATGGCGCCCCGGGCGC 1054
Oy 456	
DD 1055	5 TCCCCGCTGCCACCACGGTGATGGATTTCATCCACGTGCCTATCCTGCCTCCAATCAC 1114
Qy 469 Db 1115	9 GluileileAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLysCysA 488
Qy 488	
Db 1175	
Oy 508	8 LeuPheValGlyGlyMetCysGlnAsnCysLysAanCysPheLeuGluCysAlaTyrGln 527 :::
Db 1232	GTCGCTĠTÀĠĠĊGACTTĊCCCG
Qy 528	
Db 1268	cccaaceccaagaccaagaacataccacata
Oy 540	0

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1388 CTTGTGGCCGGTGCCAAC----- 1405
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547 LeuMet CysGlyAsnAsnAsnAsnCysCysArgCysPheCysValGluCysValAspLeuLeu 566
                                                                                                                                                                                                                                                 567 ValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspPro-TrpAsnCysTyrMetCy 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          606 nMetPhePheAlaAsnAsnHisAspGlnGluPheAspProProLys-----Va 622
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| Sequence 1. Application US/08759873
| Patent No. 5683865
| GENERAL INFORMATION:
| APPLICANT: Kaback, Dirk G. TITLE OF INVENTION: OF BREAST OR OVARIAN CANCER NUMBER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS: 14
| CORRESPONDENCE ADDRESS: NION, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W., Suite 800 CITY: Washington, D.C. COUNTRY: U.S.A. COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDUNT TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 12-APRIL-1996
CLASSIFICATION: 12-APRIL-1996
ATTORNEY APELTON: APPLICATION: AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1499 GCACCCGCCAGTGCCTCGTCTGCGTCTCCTCCTCCTCGC 1538
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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t Local Similarity:
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38-759-873-1
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53 ArgLysArgLysHisProProValGluSerGlyAspThrProLysAspProAla---- 70

368 AlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCys 387	Ş
773 TCTGAGAGCCCTCACTGGTCCGGGGCCCCAGTGAAGCCGTCTCCGCAGGCC 823	D
SerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnPr	ş
55CAGCTGCTCCCGGCC	문
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308 GlyArgIleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp 327	£ 5
04GGGACGGCAGCTGCCCCATAAAGTGCTGCCCCGGGGCCTGTCACCA	8
290 PheGlyIleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPro 307	Ş
270 GlyAspLysAsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGly 289 ::::::	음 성
	뭥
250 ProThrAspProAlaSerProThrValAlaThrThrProGluProValGlySerAspAla 269	8
\$60CCCAGCCTCCCGCCTGCGAGGTCACCAGCTCTTGGTGCCTGTTTGGC 607	Db d
238 LysValGluGluAlaSerProProAlaValGlnGln 249	Ş
506CTGGACAGTGTCTTGGACACTCTGTTGGCGCCCTCAGGTCCCGGGCAGAGCCAA 559	日
218 AlaLysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSerGln 237	Ş
198 ILESETLYSARGLYSARGASPGLUTRILEUNIANRGTRILLYSARGGLUAISGIULYSELYS 217	유 성
73 AGTTCT	B
178 SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyr 197 	δ
413 CTGTCGGACGTGGAGGCGCATATTCCAGAGCTGAAGCTACAAGGGGTGCTGGAGGCAGC 472	В
leGluSerM	δ
353 TTCCCTCGGCCCTGCCAGGGACAGGACCCCTCCGACGAAAAGACGCAGGACCAGCAGTCG 412	Дb
138 ThrProLysGluGlyArgGlyAlaProAlaGluAlaGlyLysGluGlnLysGluThrAsn 157	5
ATCTCCCTG	8
121 AlaAlaGluThrLeuProGluAlaSerArgAlaValGluAsnGlyCysCys 137	8
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101 ProGluGluGlySerProAlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGly 120	\$
176 ATGACTGAGCTGAAGGCAAAGGGTCCCCGGGGCTCCCCACGTGGCGGGCG	ф
98GluproGln 100	5
128 TCCCTCCTCCCTGGAGACGGGGGAGGAAAAGGGGAGTCCAGTCGTC 175	В
aSerGluL	Ş
68 AACACCCACTITCTCCTCCCTCTGCCCCTATAITCCCGAAACCCCCTCCTCCTTCCCTTT 127	В
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9 CGCCGCCTCCCCCCCCCCCCCCACCCAGA-GGTGGAGATCCCTCCGGTCCAGCCACATTC 67	g

뭥	24 GCTGCGGTGGAGGTTGAGGAG
3 5	88 HisasyserAsyGluSerAsyThrAlaLysAlaValGluValGluAanLysProMetil
Вb	845 GAGGATGGCTCTGAGTCCGAGGAGTCTGCGGGTCCGCTTCTGAAGGGCAAACCTCGG
Ş	408 GluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGly
ద	902GCTCTGGGTGGCGCGGCGGCTGGAGGAGGAGCCGCGGCGGCTGTCCCGCCGGGGGCC
8	422LeuGluProProGluGluLysAsnProTyrLysGluVa
В	956 GCAGCAGGAGGCGTCGCCCTGGTCCCCAAGGAAGATTCCCGCTTCTCAGCGCCCAGGGT
Ś	
В	AGGACGCGC
8	456 LysProArgLysSerThrAlaGluLys
망	1055 TCCCCGCTGGCCACCGCGTGATGGATTTCATCCACGTGCCTATCCTGCCTCTCAATCAC
Ś	469 GlullelleAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLysCysA
ф	1115 GCCTTATTGGCAGCCCGCACTCGGCAGCTGCTGGAAAGACTAACGACGGCGGGGCCC
Ş	Ile
Db	1175 GGGGCTGCCAGCGCCTTTGCCCCGCCGCGGAGTTCACCCTGTGCCTCGTCCACCCCG
Ś	yGlyMetCysGlnAsnCysLysAsnCys
ρb	1232 GTCGCTGTAGGCGACTTCCCCGACTGCGCGTACCCG
δ	528 TyrAspAspAspGlyTyrGlnSerTyrCysThrIle
дb	1268 CCCGACGCCGAGGCCCAAGGACGCGTACCCTCTATAGCGACTTCCAGCCGCCCGC
δ	540CysCysGlyGlyArgGluVa
В	1328 CTAAAGATAAAGGAGGAGGAAGGCGCGGGAGGCCTCCGCGCGCTCCCCGCGTTCCTAC
Ş	
ф	1388 CTTGTGGCCGGTGCCAAC
γŞ	
Вρ	4
γŞ	586 sGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrpProSerArgLeuG
B	1434 -GGCCACCGCCCCGCTGCCGCCGCGACCCCATCCA
Ş	606 nMetPhePheAlaAsnAsnHisAspGlnGluPheAspProProLysV
Вb	1473GACCCGGGGAAGCGGCGTGACGGC
γ	622 lTyrProProValProAlaGluLysArgLysProIleArg 635
g	rectreagrementeres
DSE DSE DSE	8 085-199B-6 ence 6, Applicatic nt No. 6235879 ERAL INFORMATION:
	LICANT: Hayden. Michael R. LICANT: Hackam, Abigail LICANT: Hug, A.H.M. Mahbubul LICANT: Chopra, Vikramjit Singh LICANT: Kalchman, Michael
	NUTTON

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118 GlyGluGly-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 GCTCAAGAGGGGAGCTGGAGGCCAAGGCCGGAGAGCTGGCCCG------CGC 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 GCAGGAGGCCTGAGCCACAGAGCAGAGCAAGTCGGAGCTGAGCTCACGGCTGGACAC 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 GluGluGluGluProArgGlyLysGluGluArgGlnGluProSerThrThrAlaArgLys 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: CDNA for Huntington-interacting protein US-09-085-1998-6
TITLE OF INVENTION: Huntington's Disease Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCES: 44
CORRESPONDENCES: ADDRESSE: ADDRESSEE: Oppedan1 & Larson
STRET: PO Box 5270
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETCE, 3.50 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORPUTER: IBM Compatible
CORPUTER: IBM COMPATER: OPPERCATING SYSTEM:
SOFTWARE: WORDER FECC.
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Matina T.
REGISTRATION NUMBER: 32038
REGISTRATION NUMBER: UBC.P-013US2
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHAX: (970) 668-2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0051
166.00
31.74%
20.82%
3.36%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: CDNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
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දු දු	118 GlyGluGly	131
ò	132 ValGluAsnGlyCysCysThrProLysGluGlyArgGlyAlaProAla	4
đ		744
δ	148 GluAlaGlyLysGluGlnLysGluThrAsnIleGluSerMetLysMetGluGlySerArg	167
а	-6	804
ò		182
q	CACCCTGGAGGAGGG	846
ò	183ArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyrIleSerLysArg	201
q		905
ò	202 LysArgAspGluTrpLeuAla-ArgTrpLys	211
q		965
ò		227
ପୁ	966 CCACCGACCCTGCCGACCGCCTCATAGACACCTGCAGGAGTGCGGGGCCCGGGCTCTGG	102
ò	ysValGluGluAlaSerProProAlaVa	247
qq	ပ	108
ò		258
qq		114
ò	258 lAlarhr	260
q	1146 TGGGCAGGAGGAGCTGGGGCCGTGGTCGACAAGGAGATGGCGGCCACATCCGCAGCCA	120
ò		266
a a	1206 TTGAAGATGCTGTGCGGAGGATTGAGGACATGATGAACCAGGCAGG	126
ò		274
엄	GGTGAACGAGAGGATCCTCAACTCCTGCACAGACCTGATGAAGGCTA	132
ò		289
a	-g	138
δ	luLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpProGlyA	309
g		143
ογ	O	324
g	1440 TCATCTCGGCCTCCAAGGCTGTGGGCTGGGAGCCACAGCTGGTGGAGGCAGCTGAC-	149
ò		344
qq	1499AAGGTGGTTCACACGGGCAAGTATGAGGAGCTCATCGTCTCGCTCCCACGAGA	155
ò	344 euMetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProM	364
g		191
δ	364 etTyrArgLysAlalleTyrGluValLeuGln	375
С	1614 CCCACCTGAGCCGCCTGCAGGATGTTCTCGCACAGTCAATGAGAGGGCTGCCAATGTGG	167

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                                                                                                                                                                                                                                                                TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MONTGOMETY, Ilene N.
REGISTRATION NUMBER: 38,97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1674 TGGCCTCCACCAAGTCAGGCCAG-----GAGCAGATTGAGGACAGAGACACCATGGATT 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1788 TGGAGCTGGAGAAGACGCTGGAGGCTGAACGCATGCGGCTGGGGGAGTTGCGGAAGCAAC 1847
                                                          HYPOTHETICAL: NANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                     MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Cosmid including AC

DESCRIPTION: promotor, ACHE gene and ARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/814,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
POSITION IN GENOME: CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 lyPheGlnProSerGlyProLysGlyLeuGluProProGluGluGluLysAsnProTyrL 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375
                                                                                                                                                                               LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
ZIP: 48334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Michigan
                                         ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysGluValTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProP 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alAlaSerSerArgAlaGlyLysLeuPheProValCysHigAspSerAspGluSerAspT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAGGTGGCCATCCGGCCCAGCACTGCCCCCCCGAAGTGTAACCACCAAGAAACCACCCC 1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Farmington Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: KOHN & ASSOCIATES 30500 No. 6025183thwestern Highway, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shani, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soreq, Hermona
Zakut, Haim
                                       Homo sapiens
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OTHER INFORMATION: /
OTHER INFORMATION: /
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FEATURE: FEATURE: Lerminator
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OTHER INFORMATION: /evid
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OTHER INFORMATION: /numb
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OTHER INFORMATION: /gene
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NAME/KEY:
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                                                                                                  FEATURE
                                                                                                                                                                                    FEATURE
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NAME/KEY:
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LOCATION:
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OTHER INFORMATION: /number= 3
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LOCATION:
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OTHER INFORMATION: /gene= "AR"
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IDENTIFICATION METHOD:
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NAME/KEY:
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27255..28007
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exon
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27385..27387
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/gene= "ACHE"
/number= 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function= "(translation start:
24110)"
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/number= 2
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/gene= "ACHE"
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                                                                                                                                                                                                                                                    /function= "arsenite resistance
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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OTHER INFORMATION: /number= 10
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COTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
US-08-814-095-7
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OTHER INFORMATION: /number= 8
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OTHER INFORMATION: /number= 13
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
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LOCATION: complement (31894..3i
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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30.88%
22.43%
3.36%
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Query Match:
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24068 AAGGG-----TGAAGGGTCGGTCGACCAGAGCCAGGGGAGGAGAGTTAGGGCACTGTCGG 24015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| ||| |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   ||| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 ProAsnGlyAspLeuGluLysArgSerGluProGlnPro-----GluGluGluGlySer 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 ProAlaGlyGlyGlyGlyGlyAlaProAlaGluGlyGluGlyAlaAla-GluThrie 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 rgGjyAlaProAlaGluAlaGjyLysGjuGlnLysGluThrAsnijeGluSerMetLysM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 etGluGly------SerArgGlyArgLeuArgGlyGlyLeuGlyTrpGluSerS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 erLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyrIleS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 erLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLysAlaL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 ysvalileAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSerGlnLysV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 al-GluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerProThrVal 258
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             GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Aiping H.
APPLICANT: LEE, Yoon S.
TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: SCOURNCES AND METHODS OF USING SAME TO MODULATE CELL
TITLE OF INVENTION: GROWTH
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SEQ ID NO 37
LENGTH: 4350
TYPE: DNA
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CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 37
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2795 AACTCCCCCGCCCCACCCCCACCCCACCCCCACCCCCAACCGCCAGACTTCCCA 2736
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                                     2915 GAATAGATCAATTGACATGAAATTTGGGGGTTCCTAATTTCTCTATGTAATTCTGCAAGT 2856
                                                                                                                 2855 CTGCTGTCAATCCTCCTGACTTTTCCATCCAAAATCTCCCGGGACCACTTCCTACCCCAG 2796
                                                                                                                                                                                                                                                                                                                                                                                                                                        2660 TCCCTAGGTGTGCTCCGGTGGGG------GGTCCCCAAGATCTTCCTTCCAGG--- 2613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2255 GGAGATGGGAACAGGAGGGGGGCTCAGACCATGGAAAACATTGGAGAATCTTAGCGGGACT 2196
                                                                                                                                                                                                                                                                                                                                                             2675 -----GACGGCCAAGATGA 2661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::: ||| :::||| 2402 CTGTCATGGTGGAAAGATTAGGCTTGGGACACACCCGCCCACCTACGGTGTAT 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2195 TTGGCCTGATCCATACAGATAT------CGTAGTTGCTTAGATATGCTTATTGTTTT 2145
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                                                                            -----ProGly 234
                                                                                                                                                        235 GluserGlnLysValGluGluAlaSerPro---ProAlaValGlnGlnProThrAspPro 253
                                                                                                                                                                                                                                       254 AlaserProThrValAlaThrThrProGluPro------ValGlySerAspAlaGly 270
                                                                                                                                                                                                                                                                                                                      271 AspLysAsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGlyPhe 290
                                                                                                                                                                                                                                                                                                                                                                                                   291 GlylleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArglle 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 LeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArg 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 LysAlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProVal 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 IleGluTrpAlaLeuGlyGlyPheGlnPro---SerGlyProLysGlyLeuGluProPro 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 GluGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGluAla 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 AlaAlaTyrAlaProProProProAlaLys------LysProArgLysSer 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387 CysHisAspSerAspGluSerAspTnrAlaLysAlaValGluValGlnAsnLysProMet 406
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532 yTyrGlnSerTyrCysThrlleCysCysGlyGlyArgGluValLeuMetCysGlyAsnAs 552
                                                                            552 nAsnCysCysArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAl 572
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hargold, Michael
APPLICANT: Hargold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Ellis, Steven
APPLICANT: Miliama, Mark
APPLICANT: McOue, Ann
APPLICANT: Miliama, Alison
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF ENQUENCES: 38
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                              LOCATION: 237..7037
OTHER INFORMATION: /standard_name= "Alpha-1A-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER:
COMPUTER:
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/290,012
FILING DATE: .11-ANG-1994
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
REPERENCE/DOCKET NUMBER: 519808
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                        ; Sequence 23, Application US/08949386; Patent No. 6090623; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08105,536
FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECULARIO (619) 230 COE2 TELEPHONE: (619) 238-0062 INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0401
161.00
29.60%
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STRANDEDNESS: double
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CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92101
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                                                                                                                                                                                                                                                                     US-08-949-386-23
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3448	89 CCGGCCAATCCAGCAGGACCTGGGCCGCCAAGACCCCACCCCTGGCAGAGGATATTGACAA	당 4
, ω	GGGCCCCAACCTGTCAACCAC	₽ ₽
272	:: ekīds	γQ
3361		Ф
252	oThrAsp	Ş
232 3316	218 AlaLysVal	g 8
3259	3206 CCGGGCGCGAGGGCGAGGGCGAGGGCCCCGACGGGGGCGAGCGCAGGAGAAG	Ъ
₩.	98 IleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLys	δ
3205	3173 GAGGGCGCGCACCGCGA	당
197	ProArgLeuThrPheGlnAlaGlyAspProTyrTyr	ογ
3172	13 TCGACGTCATCGCGCGCACCGCAGGCCCCGGGGAGGACGACGACCGAGGACCG	문 4
1 77		?
157 3112	149 AlaGlyLysGluGlnLysGluThrAsn	용 성
3052	CACCG	망
148	•	Ş
3013	2969 GGGCAGCCTGGAGCAACCCGGGTTCTGGGAGGGCGAGGCCGAGCG	밁
132	SerArgAlaVal	Ş
2968	2918 GCTGAGCCGGGAGCCCTACGGCCGCGAGTCGGACCACCACGCCCGGGA	망
112		ş
2917	2858 CCCCAGCGGCTCGGCGGGCCTGGACGCACGGAGGCCCTGGGCGGGAAGCCAGGAGGCCGA	Db
92	roSerMetAlaGlnAspSerGlyAlaSerGluLeuLeuProAsnGlyAsp	ş
2857	GGGCCCGGGA	DЬ
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2812		정
55		δ
2752	6 GACGCACTTGGACCGGCCGGTGGTGGTGGTGGACCCGCAGGAGAACCGCAACAACAACAC	DЪ
37		δ
21 2695	7 SerGlyProGlyAspThrSerSerSerAlaAlaGluArgGluGlu :::	ß &
	-720-086-7 (1-912) x US-08-949-386-23 (1-7791)	US-09
	Local Similarity: 20.52% · Mismatches: 234 / Match: 3.26% Indels: 334 / Gaps: 41	Best L Query DB:

4057	98 CATGGTCATTGCCATGAGCAGCATCGCCCTGGCCCGAGGACCCTGTGCAGCCCAACGC	Db 39
635	/sArgLysProlleArg	Qy 6
3997	CTACTTTGAGATGTGCATCCT	Db 39
628	16 GluPheAspProProLysValTyrProProValProAla	δ Q
3937	CCTCCCTATAGCTCCATGTTCATCCTGTCCACGACCAA	Db 38
615	erArgLeuGlnMetPhePheAlaAsnAsnHisAspGln	Qy 5
3880	GGGA	Db 38
595	576 IleLysGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeu	Оу 5
3871		Db 3871
575	56 ArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAla	Ωу 5
3871	860GGAGGAAGACGA	Db 38
555	lLeuMetCysGlyAsnAsnAsnCysCys	Qy 5
3859	9	Db 385
535	516 AsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSer	Qy 5
3859	4	Db 385
515	496 SerCysGlySerLeuAsnValThrLeuGluHisProLeuPheValGlyGlyMetCysGln	Qy 4
3853	GAGAAGAA	Db 38
495	476 ArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAspIleCysIle	Qy 4
3844		Db 37
475		0у 4
3784	725 TGCCAGGAAACCCGACCACACCACAGTGGACATCCCCCCAGCCTGCCCACCCCCCCTCAA	Db 37
455		Qy 4
3724	TTATCGTCACCAACCCCAGCGGCACCCAGACCAATTCAGCTAAGAC	Db 36
440		Qy 4
3664	26CAACCCGGGGAACCCATCCAATCCCGGCCCCCCCAAGAC	Db 36
427	ProSerGlyProLysGlyLeuGluProProGluGlu	0у 4
3625	TGGCCACCAACCCCCAGAACGCCGCCAGCCGGACGCCCAA	Db 35
407	lnAsnLysProMetIle	Оу з
3580	CCCTGC	Db 35
387	68 AlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCys	Оу з
3562	CC	Db 35
367	ProMetTyrArgLys	Qy 3
3544	36	Db 35
347	rValValCysValGlubysLeuMetProLeu	Qy 3
3535	09	35
327	08 GlyArgIleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp	Qy 3

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4058 ACCTCGGAACAACGTGCTGCGATACTTTGACTACGTTTTTACAGGCGTCTTCACCTTT-- 4115
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                                                                                                                                                                                                                                                            4116 -----GÄĞATGGTGATCÄAGATGATTGA 4138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4193 -CGACTTCATAGTGGTCAGTGGGCCCT-------GGTAGCCTTTGCCT 4233
636 -------ValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLy 651
                                                                                                                                                                      651 sAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValCysGluAspSerIleTh 671
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APPLICANT: Harpold, Michael
APPLICANT: Harpold, Milliams, Mark
APPLICANT: Williams, Mark
APPLICANT: MCCUe, Ann
APPLICANT: Feldman, Daniel
APPLICANT: Feldman, Daniel
APPLICANT: Feldman, Daniel
APPLICANT: Feldman, Millson
APPLICANT: Feldman, Millson
APPLICANT: Moveration and APPLICANT: AND APPLICANT: APPLICANT: Red Millson
APPLICANT: A
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1660 Union Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-SEPT-1994
PRICK APPLICATION DATE: 28-SEPT-1994
PRICK APLICATION NUMBER: 08/31,363
PRIOR APLICATION DATA: 08/31,363
PRIOR APLICATION DATA: 08/290,012
PRICK APPLICATION DATA: 08/290,012
PRICK APPLICATION DATA: 08/294
PRICK APPLICATION DATA: 4-APR-1994
PRICK DATE: 4-APR-1994
PRICK DATE: 4-APR-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/336,257
FILING DATE: 7-NOV-1994
APPLICATION DATA:
APPLICATION NUMBER: 08/336,257
APPLICATION NUMBER: 08/314,083
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08450562 Patent No. 6096514
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28-SEPT-1994
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California
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| PRIOR DATE | 07/1914 | 097 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 | 19810 |
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TyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCys 387	368 AlaileTy	δ
	3545	ф
PheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys 367	348 SerSerPh	ş
GATGGGAAA 3544	3536	뮍
TrpPhe	328 ValMetTr	8
	3509	뭥
eValSerTrpTrpMetThrGly	308 GlyArgIl	γQ
TCCCCACGGCAGCCT	3449 CATGAAGA	망
GlyGluLeuValTrpGlyLysLeuArqGlyPheSerTrpTrpPro 307	293 GlyGluLe	Ş
CCGGCCAATCCAGCAGGACCTGGCCGCCAAGACCCCCTGGCAGAGGATATTGACAA 3448	-	gg s
ThrivsAlaGlvAspAspGluProGluTvrGluAspGlvAroGlvPheGlvIle 292	273 AsnAlaTh	Ş
SerProThrValAlaThrThrProGluProValGlySerAspAlaGlyAspLys 272	253 ProAlaSe	P 64
GCGGAGGCATCGGAGGAGGAAGAAGAACCAGGGCTCCGGGGTCCC 3361	317	DЬ
GluSerGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAsp 252	233 ProGlyGluS	γQ
TGGCGCTCCAGCCAC	3260 GCACCGGC	DЬ
ValIleAlaGlyMetAsnAlaValGluGluAsnGlnGly 232	218 AlaLysVal	Ş
ccgagacaacaacaacaacaacaacaacaacaacaacaac	3206 CCGGGGCG	Вb
LysargLysargaspGluTrpLeuAlaargTrpLysargGluAlaGluLysLys 217	198 IleSerLy	Ş
AGGGCGCGCACCGCGA	3173 GAGGGCGC	망
LeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyr 197	178 SerSerLe	Ş
TCGACGTCATCGCGCGCACCGCAGGCCCCGGGGAGGAGGACGAGGACAAGGCGGAGCG 3172	3113 TCGACGTC	망
SerMetLyaMetGluGlySerArqGlyArgLeuArgGlyGlyLeuGlyTrpGlu 177	158 IleGluSe	Ş
:::	3053 GCAGGGGG	đđ
LysGluGlnLysGluThrAsn 157	149 AlaGlyLy	γQ
AGGCAAGGCCGGGGACCCCCACCGGAGGCACGTGCACCG 3052	3014	Вb
luAsnGlyCysCysThrProLysGluGlyArgGlyAlaProAlaGlu 148	133 GluAsnGl	ş
GGGCAGCCTGGAGCAACCCGGGTTCTGGGAGGGCGAGGCCGAGCG 3013		Db.
ProAlaGluGlvGluGlvAlaAlaGluThrLeuProGluAlaSerArgAlaVal 132	ll3 GlyAlaPr	Q V
GCTGAGCCGGGAGGGACCCTACGGCCGCGAGTCGGACCACGCCCGGGA 2968	2918 GCTGAGCC	Дb
LysArgSerGluProGlnProGluGluGlySerProAlaGlyGlyGlnLysGly 112	93 LeuGluLy	Ş
:::	2858 CCCCAGCG	Db
roSerMetAlaGlnAspSerGlyAlaSerGluLeuLeuProAsnGlyAsp 92	76 ProSerMe	Ş
GGACTTCCTCAGGAAACAGGCCCGCTACCACGATCGGGCCCGGGA 2857	2813 GGACTTCC	Вb
ProProValGluSerGlyAspThrProLysAspProAlaValIleSerLysSer 75	56 LysHisPr	ş
CAACAAGAGCCGGGCGGACCGACCGTGGACCAGCGCCTCGGCCAGCAGCAGCGCGCCGA 2812	ω	뮹 !
GluProSerThrThrAlaArgLysValGlyArgProGlyArgLysArg 55	38 ArgGlnGl	Ş

711	rGlnLysHisIleGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAs	691	δ
4192	ccTGGGGCTCGTGCATCAGGGTGCCTACTTCCGTGACCTCTGGAATA	4139	ф
691	н	671	γQ
4138		4116	Дb
671	sAspLeuGlyIleGlnValAspArgTyrIleAlaSer	651	Qy
4115	ACCTCGGAACAACGTGCTGCGATACTTTGA	4058	Db
651	ValLeuSerLeupheAs	636	Qy
4057		3998	da
635		629	γQ
3997	CCCCCTTCGCCGCCTGTGCCATTACATCCTGAACCTGCGCTACTTTGAGATGTGCATCCT	3938	ДD
628	GluPheAspProProLysValTyrProProValProAla	616	Qy
3937	AGACGGCCCTAAGCCAATGCCTCCCTATAGCTTCATCCTGTCCACGACCAA	3881	Db
615	ArgArgArgGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsnHisAspGln	596	γQ
3880		3872	쁄
595	: IleLysGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeu	576	γQ
3871		3871	В
575	ArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAla	556	γQ
3871	GGAGGAAGACGA	3860	DЪ
555	TyrCysThrIleCysCy	536	δλ S
3859		3859	Db
535	AsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSer	516	γQ
3859		3854	дb
515	SerCysGlySerLeuAsnValThrLeuGluHisProLeuPheValGlyGlyMetCysGln	496	γ
3853	AGAGAAGAA	3845	4 0
495	ArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAspIleCysIle	476	9
3844	CCACACCGTCGTACAAGTGAACAAAAAACGCCAACCCAGACCCACTGCCAAAAAAAA	3785	đđ
475	ProLysValLysGluIleIleAspGl	456	Ş
7	CAGCCTGCCCACCCCCCTCA	3725	Db .
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407 3625	HisAspSerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLysProMetIle	388	B 성
3580		3563	Db Db

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2918 GCTGAGCCGGGAGGACCCTACGGCCGCGAGTCGGACCACCA-----CGCCCGGGA 2968
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                                                                                 2753 CAACAAGAGCCGGCCGGCCGACCCACCGTGGACCAGCGCCTCGGCCAGCAGCGCGCCGA 2812
                                                                                                                                                            2813 GGACTICCICAG----GAAACAGGCCGCTACCACGATCG--------GGCCCGGGA 2857
                                                                                                                                                                                                                                        3014 -------AGGCAAGGCAAGGCCGGGGGACCCCCACCGGAGGCACGTGCACCG 3052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3206 ccagaccaccacaagaccaagaccaccaaccaccacacaa-----ccacagaaaaa 3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3317 ------GCGGAGGCATCGGAGGAAGAGAAGAGAACAGGCTCCGGGGTCCC---- 3361
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  2696 GACGCACTTGGACCGGCCGCTGGTGGTGGACCCGCAGGAGAACCGCAA---CAACAACAC 2752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3449 CATGAAGAACAAGCTGGCCACCGGGGAGTCGGCCGCTCCCCACGGCAGCCTTGGCCA 3508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3536 -----GATGGGAAA-----3544
                                                                                                                                                                                                                                                                                        93 LeuGluLysArgSerGluProGlnProGluGluGlySerProAlaGlyGlyGlnLysGly 112
                                                                                                                                                                                                                                                                                                                                                                          113 GlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLeuProGluAlaSerArgAlaVal 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 GluAsnGlyCysCysThrProLysGluGlyArgGlyAlaProAlaGlu------ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 IleGluSerMetLysmetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyr 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 IleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLys 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 ProGlyGluSerGlnLysValGluGluGluAlaSerProProAlaValGlnGlnProThrAsp 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 AlaLysVal------IleAlaGlyMetAsnAlaValGluGluAsnGlnGly 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 ProhlaSerProThrValAlaThrThrProGluProValGlySerAspAlaGlyAspLys 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 AsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIle 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 GlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrp--------rjrpPro 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeu 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 GlyArgIleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp 327
                                        38 ArgGlnGluProSerThrThrAlaArgLy8-----ValGlyArgProGlyArgLy8Arg 55
                                                                                                                          56 LysHisProProValGluSerGlyAspThrProLysAspProAlaValIleSerLysSer 75
                                                                                                                                                                                                         76 ProSerMetAlaGlnAspSerGlyAlaSerGluLeuLeu-----ProAsnGlyAsp 92
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                                                                4234 -TCACTGGCAATAGCAAAGGAAAAGACATCAACACGATTAAATCCCTCCGAGTCCTCCGG 4292
------GGTAGCCTTTGCCT 4233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2636 AATGGACCCGGACGAGCGCTGGAAGGCTGCCTACACGCGGCACCTGCGGCCAGGACATGAA 2695
                                        711 nAspLeuSerIle----LysGl 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 Asp------ArgLysAspGlyGluGluGluGluGluProArgGlyLysGluGlu 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 SerGlyProGlyAspThr-----SerSerSerAlaAlaGluArgGluGlu 21
                                                                                                                                                                                                                        US-06-984-709A-23
Sequence 23, Application US/08984709A
Sequence 23, Application US/08984709A
Secuence 10. 632003C
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND TITLE OF INVENTION: METHODS
NUMBER OF SECUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REPERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /standard_name= "Alpha-lA-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                             STREE: Heller Ehrman White & McAuliffe STREE: 4250 Executive Square, Suite 700 CITY: La Jolla STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTR:

ZIP: 92037

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
4193 -CGACTTCATAGTGGTCAGTGGGGCCCT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (619) 450-840
TELEPAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7791 base pairs
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20.52%
3.26%
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TRANDEDNESS: double
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Query Match:
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Pred. No.:
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¥	368	AlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCys 387	
ਰੱ	3563	CATGCTGGCATCCCTGC 3580	
₹	388	isAspSerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLys 	
ਲੋ	3581	CATGGCCACCAACCCCCAGAACGCCGCCAGCCGGCCGGACGCCCAA 3625	
₹	408	GluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGlu 427	
ğ	3626	CAACCCGGGGAACCCATCCAATCCCGGCCCCCCAAGAC 3664	
₹	428	GluLysAsnProTyrLys	
ğ	3665	CCCCGAGAATAGCCTTATCGTCACCAACCCCAGCGGCACCCAGACCAATTCAGCTAAGAC 3724	
Ž	441	ValGluProGluAlaAlaAlaTyrAlaProProProProAlaLys 455	
ŏ	3725	TGCCAGGAAACCCGACCACAGTGGACATCCCCCCAGCCTGCCCACCCCCCCTCAA 3784	
¥	456	LysProArgLysSerThrAlaGluLysProLysValLysGluIleIleAspGluArgThr 475	
ğ	3785	CCACACCGTCGTACAAGTGAACAAAAACGCCAACCCAGACCCACTGCCAAAAAAAA	
₹	476	ArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAspIleCysIle 495	
₽.	3845	AGAGAAGAA 3853	
₹	496	SerCysGlySerLeuAsnValThrLeuGluHisBroLeuPheValGlyGlyMetCysGln 515	
ŏ	3854	3859	
₹	516	AsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSer 535	
ğ	3859	3859	
¥	536	TyrCysThrIleCysCysGlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCys 555	
ğ	3860		
¥	556	ArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAla 575	
ğ	3871	3871	
Š	576	<pre>IleLysGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeu 595</pre>	
ŏ	3872		
¥	596	isAsp	
ğ	3881	AGACGGCCTAAGCCAATGCCTCCTATAGCTCCATGTTCATCCTGTCCACGACCAA 3937	
¥	616	GluPheAspProProLysValTyrProProValProAla628	
岁	3938	CCCCCTTCGCCGCCTGTGCCATTACATCCTGAACCTGCGCTACTTTGAGATGTGCATCCT 3997	
ž	629		
ğ	3998	CATGGTCATTGCCATGAGCAGCATCGCCCTGGCCGCCGAGGACCCTGTGCAGCCCAACGC 4057	
¥	636	ValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLy 651	
ğ	4058	ACCTCGGAACAACGTGCTGCGATACTTTGACTACGTTTTTACAGGCGTCTTCACCTTT 4115	
₹	651	eAlaSerGluVa	
ğ	4116	GAGATGGTGATCAAGATGATTGA 4138	
¥	671	rValGlyMetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValTh 691	
6	4139	CCTGGGGCTCGTCCTGCATCAGGGTGCCTACTTCCGTGACCTCTGGAATATTCT 4192	

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,272
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/336,257
FILING DATE: 13-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,083
FILING DATE: 28-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,363
FILING DATE: 28-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,363
FILING DATE: 23-SEPT-1994
PRIOR APPLICATION: 435
PRIOR DATE: 23-SEPT-1994
PRIOR APPLICATION: 435
PRIOR DATE: 23-SEPT-1994
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APPLICATION NUMBER: 08/290,012
FILLING DATE: 11-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILLING DATE: 4-APR-1994
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193,078
FILLING DATE: 07-FEB-1994
FILLING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPLICATION UNMERE: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION UNATA:
RAPLICATION UNMERE: 08/105,536
FILING DATE: 11-AUG-1993
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APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4193 -CGACTTCATAGTGGTCAGTGGGGCCCT--------GGTAGCCTTTGCCT 4233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4234 -TCACTGGCAATAGCAAAAGGAAAAGACATCAACACGATTAÁATCCCTCCGAGTCCTCCGG 4292
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CITY: San Diego
STATE: California
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Gillespie, Alison
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Ellis, Steven
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2918 GCTGAGCCGGGAGGGACCTTACGGCCGCGAGTCGGACCACCA-----CGCCCGGGA 2968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 Asp-----ArgLysAspGlyGluGluGluGluGluProArgGlyLysGluGlu 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 LysHisProProValGluSerGlyAspThrProLysAspProAlaVallleSerLysSer 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 SerGlyProGlyAspThr-----SerSerSerAlaAlaGluArgGluGlu 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 237..7037
OTHER INFORMATION: /standard_name= "Alpha-lA-2"
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:

APPLICATION WIBER: 07/914,231
FILING DATE: 13-ULX-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: 10-APR-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/86,354
FILING DATE: 11-ANG-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-ANG-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-ANG-1991
CLASSIFICATION: 35-ANG-1991
CLASSIFICATION: 35-ANG-1991
CLASSIFICATION: 35-ANG-1991
CLASSIFICATION: 55-ANG-1991
CLASSIFICATION: 55-ANG-1991
TELEFANION NUMBER: 33,779
TELEFANION FOR SEQ 1D NO: 23:
FELEPANION FOR SEQ 1D NO: 23:
FENDENMENT TABLEFARFICE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 7791 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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161.00
29.60%
20.52%
3.26%
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Query Match:
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Pred. No.:
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qq	CCGGGGACCCCCACCGGAGGCACGTGCACCG	3052
ò	9 AlaGlyLýsGluGlnLysGluThrAsn	157
qa		3112
ò	<pre>8 IleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu 1 </pre>	177
셤	3 TCGACGTCATCGCGCGCACCGCAGGCCCGGGGAGGAGGGTCCGGAGGACAAGGCGGAGCG 3	3172
ò	178 SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyr 1.	197
g		3205
ò	198 IleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLys 2	217
qq	m	3259
ò	218 AlaLysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGly 2.	232
q		3316
ò	233 ProGlyGluSerGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAsp 2:	252
q		3361
ò	253 ProAlaSerProThrValAlaThrThrProGluProValGlySerAspAlaGlyAspLys 2'	272
q	AACCAC	3388
ò	273 AsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIle 2:	292
g		3448
ò	c	101
qq	AAGCTGGCCACCGCTCCCCACGGCAGCCTTGGCCA 3	508
ò	308 GlyArglleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp 3.	327
q		3535
ò	328 ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeu 34	347
q		3544
ò	348 SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys 36	367
qq	'n	1562
ò	368 AlaileTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCys 38	187
qa	cccTGC 3	1580
ò	388 HisAspSerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLysProMetIle 4(407
q		3625
ò	408 GluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGlu 43	427
q	Ю	1664
ò	428 GluLysAsnProTyrLysGluValTyrThrAspMetTrp 44	0
q		3724
ò	441ValGluProGluAlaAlaAlaTyrAlaProProProProAlaLys 46	455
qq		3784

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RESULT 15
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                                                                  Sequence 22, Applicat: Patent No. 6090623
GENERAL INFORMATION:
                  APPLICANT:
APPLICANT:
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 APPLICANT:
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                                                                                                                                                                                                                                                   - TCACTGGCAATAGCAAAGGAAAAGACATCAACACGATTAAATCCCTCCGAGTCCTCCGG
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                                                                                                      Application US/08949386
                  Harpold, Michael
Ellis, Steven
Williams, Mark
McCue, Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-949-386-22
                                                                                                                                                                                                                                                                                  US-09-720-086-7 (1-912) x US-08-949-386-22 (1-7808)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 08/14;
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gillespie, Alison
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
2813 GGACTTCCTCAG---GAAACAGGCCCGCTACCACGATCG-----
                                                                     2753 CAACAAGAGCCGGGCCGAGCCCACCGTGGACCAGCGCCTCGGCCAGCAGCGCGCCGA
                                                                                                                                                                                                               2636 AATGGACCCGGACGAGCGCTGGAAGGCTGCCTACACGCGGCACCTGCGGCCAGACATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 519808
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/949,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                        2696 GACGCACTTGGACCGGCCGCTGGTGGTGGACCCGCAGGAGAACCGCAA---CAACAACAC 2752
                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 237..776
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                               38 ArgGlnGluProSerThrThrAlaArgLys-----ValGlyArgProGlyArgLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                           22 Asp------ArgLysAspGlyGluGluGluGluFroArgGlyLysGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                              7 SerGlyProGlyAspThr---
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                             LysHisProProValGluSerGlyAspThrProLysAspProAlaValIleSerLysSer
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1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7808 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (619)
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상 임	Qy 76 ProSerMetAlaGlnAspSerGlyAlaSerĞluLeuLeuProAsnGlyAsp 92	-	
ò	93 LeuGluLysArgSerGluProGlnProGluGluGlySerProAlaGlyGlyGlnLysGly		
g	2918 GCTGAGCCGGGAGGGACCCTACGGCCGCGAGTCGGACCACCACGCCCGGGA		
දු ද	Oy 113 GlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLeuProGluAlaSerArgAlaVal 132 Db 2969 GGGCAGCCTGGAGCAACCCGGGTTCTGGGAGGGGGGGGGG		
ò	133	-	
qq	Db 3014AGGCAGGGGGGGCCGGGGACCCCACCGGAGGCACGTGCACCG 3052		
ò	149 AladlyLysGluGlnLysGluThrAsn	_	
qq	1051 GCAGGGGCAGCAGGGAGAGCCGCAGCGGGTCCCCGCGCGCG		
ò	158 IleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu		
qq	3113		
ò	178 SerSerLeuArgGlnArgProMetProArgLeuThrPheGl		
qq	3173		
ò	198 IleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysAr		
qq	3206		
ઠે	218		
р	Db 3260 GCACCGGCATGGCGCTCCAGCCACGTACGAGGGGACGCGCGGAGGGAGGAGGACAAGGA 3316		
ò	233		
g	Db 3317GCGGAGGCATCGGAGGAAAGAAGAACCACGGGCTCCGGGGTCCC 3361		
ò	Qy 253 ProAlaSerProThrValAlaThrThrProGluProValGlySerAspAlaGlyAspLys 272		
Ωp	3362		
ò	273		
QQ	3389		
ઠે	293		
Q	Db 3449 CATGAAGAACAACAAGCTGGCCACCGCGGGGGCGCCGCTCCCCACGGCAGCCTTGGCCA 3508		
ò	308		
QQ	Db 35093535		
ò	Qy 328 ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeu 347		
qq	3536		
ò	348 SerSerPheCysSerAlaPheHisGlnAl		
QQ	Db 3545 3562	•	
ò	368 AlalleTyrGluValLeuGlnValAlaSer		
QQ	Db 3563CATGCTGGCCATCCTGC 3580	-	
ò	388		
qq	Db 3581 CATGGCCACCAACCCCCAGAACGCCGCCAGCCGCCGGACGCCCCAA 3625		

à	408	LeuGluProProGluGI	427
q	3626	CAACCGGGGAACCATCCAATCCCGGCCCCCCCAAGAC	3664
ò	428	GluLysAsnProTyrLysGluValTyrThrAspMetTrp	440
gg	3665	ccccaagaatagcctriatcatcaccaacccaacccaaccaacaatrcagctaagac	3724
ò	441	ValGluProGluAlaAlaAyrAlaProValGluProProAlaLyB	455
Ωp	3725	crecchecce	3784
ò	456	LysProArgLysSerThrAlaGluLysProLysValLysGluIleIleAspGluArgThr	475
g	3785	ccerocaagigaacaaaaaacccaacccaagacccacigc	3844
ò	476	ArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAspIleCysIle	495
g	3845	AGAGAAGAA	3853
ò	496	SerCysGlySerLeuAsnValThrLeuGluHisProLeuPheValGlyGlyMetCysGln	515
Op	3854		3859
ò	516	$\tt AsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSer$	535
q	3859		3859
ò	536	TyrCysThrIleCysCysGlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCys	555
а	3860		3871
ò	556	ArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAla	575
qq	3871		3871
ò	576	IleLysGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeu	595
g	3872	CCGTGGGGA	3880
ò	596	ArgArgArgGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsnHisAspGln	615
g	3881	AGACGGCCCTAAGCCAATGCCTCCCTATAGCTCCATGTTCATCCTGTCCACGAACGA	3937
ò	919	GluPheAspProProLysValTyrProProValProAla	628
q	3938	CCCCCTTCGCCGCCTGTGCCATTACATCCTGGAACCTGCGCTACTTTGAGATGTGCATCCT	3997
ò	629		635
QQ	3998	CATGGTCATTGCCATGAGCAGCATCGCCCTGCCGAGGACCCTGTGCAGCCCCAACGC	4057
ò	636	ValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLy	651
g	4058	ACCTCGGAACAACGTGCTGCGATACTTTGACTACGTTTTTTACAGGCGTCTTCACCTTT	4115
ò	651	sAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValCysGluAspSerIleTh	671
QQ	4116		4138
ò	671	rValGlyMetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValTh	691
g	4139	CTGGGGCTCGTCCTGCATCAGGGTGCCTACTTCCGTGACCTCTGGAATATTCT	4192
ò	691	rGlnLysHisIleGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAs	711
g	4193	CCTGGTAGCCTTTG	4233
ò	711	nAspLeuSerIleLysGl	722
qq	4234	-TCACTGGCAATAGCAAAAGACATCAACACGATTAAATCCCTCCGAGTCCTCCGG	4292
ò	722	yLeuTyrGlu 725	

Db 4293 GTGCTACGAC 4302

Search completed: November 25, 2002, 02:59:49 Job time: 272.557 secs

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REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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ORGANISM
             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                       Alignment Scores:
                                                               Score:
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Direct Submission
Submitted (J5-MAY-1998) CVRC, Mass. Ge
Street, Charlestown, MA 02129, USA
3 (bases 1 to 3005)
Hata, K., Shirohau, H., Sasaki, H. and Er
Direct Submission
Submitted (12-FEB-2001) CVRC, Mass. Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens DNA complete cds.
AF067972
AF067972.2 GI:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-FEB-2001) CVRC, Mass. Ge
Street, Charlestown, MA 02129, USA
Sequence update by submitter
On Feb 12, 2001 this sequence version
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning, expression and gene family Gene 236 (1), 87-95 (199 99365304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eucheria; Primates; Catarrhini; Hominidae.
1 (bases 1 to 3005)
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                                                                                                                      ARKVGRPGRKRKHPPUSGGPGDTSSSAAEREEDRKDGEEQEEPRGKEERQEPSTT
ARKVGRPGRKRKHPPUSGGPTPKDPAVISKS PSMAQDSGASELLPNGDLEKRSEPQPE
EGSPAGGOKGGA PAFGEGAAETLPEASRAVENGCCTPKEGRGAPAEAGKEOKETNIES
MKMEGSBGRLRGGLGMESSLRQRPMPRLTFQAGDPYYISKRKDEWLARWKREAEKKA
KVIAGMNAVEERQGPGBSOKVEEASPPAAVQOPTDPASFTVATTPEPVGSDAGDKNATK
AGDDEPEYEDGRFGIGELVWGKLRGFSWMFGRIYEVLCVASSRAGKLFPVCHDSDE
STAKAVEVONKEMIEWALGGFQPSGPKGLEPPEEKHPYKEVYTDMWVEPEAAYAP
PPPAKKCPNCKNCFLECAYQYDDDGYQSYCTICCGGREVLMCGNNNCCRCFCVECVDLL
VGPGAAQAAIKEDPMNCYMCGHKGTYGLLRRREDPSECKHPYKEVYTDMWVEPEAAYAP
PVPARKKKPIRVLSLFDGIATGLLVLKDLGIQVDVIJASEVCEDSITVGMVRHQGKIM
YVGDVBSVTQKHIQEWGFFDLVUGGSPCNDLSINPARKGLYEGGRLFFEFYRLLHD
ARPKEGDDRFFFWLFENVVAMGVSDKRDISTINFARKGLYEGGRLFFEFYRLLHD
PARKENDLSTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKQKOGKDQHFPVFMNEKE
DILWCTEMERVVGFPULYDGSSDKRDISTINFARKGLYSGAAHRARYFWGNL
PGMNRPLASTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKQKOGKDQHFPVFMNEKE
DILWCTEMERVFGFPULYTDVSMMSRLARQRLLGRSWSVFVIRHLFAPLKEYFACV*

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/gene="DNMT3A"
                                                                                                                                                                                                                                                                                                                                         /product="DNA cytosine methyltransferase 3 alpha"
/protein_id="AAD33084.2"
/db_xref="GI:12746532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                            function="de novo
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          Length:
Matches:
Conservative:
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Gaps:
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GluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLeu 300
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GTTGAGAAGCTGATGCCGCTGAGCTCGTTTTGCAGTGCGTT
                       ValGluLysLeuMetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsn
                                                                                                               AlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLysPheSerValValCys
                                                                                                                                                                                                    ArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMetThrGlyArgSerArg
                                                                                                                                                                                                                                                                      GAGCCAGAGTACGAGGACGGCCGGGGGCTTTGGCATTGGGGAGCTGGTGTGGGGGAAACTG
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                                                                                     GCAGCTGAAGGCACCCGCTGGGTCATGTGGTTCGGAGACGGCAAATTCTCAGTGGTGTGT
                                                                                                                                                                               CGGGGCTTCTCCTGGTGGCCAGGCCGCATTGTGTCTTGGTGGATGACGGGCCGGAGCCGA
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ર્ გ 8 ঠ 8 হ β, 밁 á 밁 ş Ś 밁 밁 á 유 Ś 문 ફ ર્ 용 용 Ş Ś 밁 á 몽 á 밁 ŏ ð 밁 Ş 맑 203 1970 1790 1730 1610 1550 1490 1430 1370 1310 2090 1910 1850 1670 2150 2330 2210 521 46 441 421 401 381 661 6 541 501 481 361 641 621 581 561 701 ValGluproGluAlaAlaAlaTyrAlaProProProProAlaLysLysProArgLysSer ValGlnAsnLysProMetIleGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLys GlyLysLeuPheProValCysHisAspSerAspGluSerAspThrAlaLysAlaValGlu CysGlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysVal GlyLeuGluProProGluGluGluLysAsnProTyrLysGluValTyrThrAspMetTrp PheAspLeuValIleGlyGlySerProCysAsnAspLeuSerIleValAsnProAlaArg IleAlaSerGluValCysGluAspSerIleThrValGlyMetValArgHisGlnGlyLys TrpAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAsp GAGTGTGTGGACCTCTTGGTGGGGCCCGGGGGCTGCCCAGGCAGCCATTAAGGAAGACCCC GluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspPro GGCCTGGAGCCACCAGAAGAAGAAGAATCCCTACAAAGAAGTGTACACGGACATGTGG IleMetTyrValGlyAspValArgSerValThrGlnLysHisIleGlnGluTrpGlyPro #AlaGluLy8ProLy8ValLy8GluIleIleAspGluArgThrArgGluArgLeuVal TPPTOSerArgLeuGlmMetPhePheAlaAsnAsnHisAspGlnGluPheAspProPro 1909 560 1849 1789 520 500 1669 480 1609 460 1549 440 1489 420 2329 580 540 2269 680 2209 660 2089 2029 1969 700 2149 640 620 600

> RESULT 2 AF331856 á 5 á Ş ð 밁 á 밁 Ş δ 밁 ર્ 문 5 밁 В В 밁 밁 2930 2750 2690 2570 2510 2450 2810 901 881 198 801 781 761 741 721 LysGlnGlyLysAspGlnHisPheProValPheMetAsnGluLysGluAsp!leLeuTrp HisGlyArgIleAlaLysPheSerLysValArgThrIleThrThrArgSerAsnSerIle MetGlyValSerAspLysArgAspIleSerArgPheLeuGluSerAsnProValMetIle AlaArgProLyeGluGlyAspAspAspProPhePheTrpLeuPheGluAsnValValAla LysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrArgLeuLsullisAsp LeuPheAlaProLeuLysGluTyrPheAlaCysVal SerArgLeuAlaArgGlnArgLeuGlyArgSerTrpSerValProValIleArgHs AGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGGTCATGGAGCGTGCCAGTCATCCGCCAC ag 912 **TRNA** ב ב 2869 2809 2740 0.40 2689 750 2449 960 383

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Sequence 47, Application US/09276531

Sequence 47, Application US/09276531

Sequence 47, Application US/09276531

Patent No. 6183968

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
ICANT: Reddy, Roopa
ICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
ITILE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
INVESER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         000
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MEDIUM TYPE: Floppy disk
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NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-00
REFERENCE/DOCKET NUMBER: PA-00
REFERENCE/DOCKET NUMBER: PA-00
RELECOMMUNICATION IMPORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTTUTO2
CLONE: 1271435
US-09-276-531-47
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Query Match:
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                                                    AAGCTGCTGGGAAGGTCCTGGAGCGTGCCTGTCATCCGACACCTCTTCGCCCCCTCTGAAG
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RESULT 2 US-08-913-832A-1

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Maximum I
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09720086/runat_18112002_092957_29457/app_query.fasta_1.4252
-Q=/cgn2_1/USPTO_spool/US09720086/runat_18112002_092957_29457/app_query.fasta_1.4252
-DB=Issued_patents_NA_-CMT**Eastap_-SUPFTX=rri -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0-UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=sct -HEAPSIZE=500
-MODE=LOCAL -OUTFMT=pto -NORM-sct +HEAPSIZE=500 -MAINLEN=0 -MAXLEN=200000000
-USER=US09720086 @CGN 1 1 108 @runat 18112002_092957_29457 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-913-832A-1

US-09-249-181A-1

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US-08-913-159-12

US-08-962-284-1

US-08-931-999-4

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Sequence 1, Appli	Sequence 11, Appl	11,	1,	Sequence 1, Appli	1,	,	e 1,	13	e 1, A	14	14,	w	Sequence 5, Appli	e 16,	e 16,	e 1,	е 3, Арр	3, Appl	e 3, Appl	e 1, Appl	Sequence 1, Appli	2,	36,	e 2, App	Sequence 2, Appli	e 2, Appl	e 1, App	1, App	1, App	Sequence 5, Appli	1, App	Sequence 1, Appli

ALIGNMENTS

US-09-276-531-47 Patent No.

Sequence 47, Application US/09276531

6183968

GENERAL INFORMATION:

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APPLICANT:
APPLICANT:
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACH
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

NUMBER OF SEQUENCES: 134
ATTORNEY/AGENT INFORMATION:
                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                   APPLICATION NUMBER: 60/079, FILING DATE: March 27, 1998
                                                                                                 CLASSIFICATION:
                                                                                                                      APPLICATION NUMBER: FILING DATE: Herewi
                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                     COUNTRY:
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61 AGG---CGGCTCTTCTTCTCTTTC-CACCTGCTGAATTACTCACGCCCCAAGGAGGGT 116
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Lynn E. Murry, Ph.D.
REGISTRATION UNDRER: 42 918
REFERENCE/DOCKET NUMBER: 9A-0008 US
TELECOMMUNICATION INFORMATION:
TELEFONE: (650) 845-0555
TELEFAX: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIMEDARY: TESTIVO2
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                                               APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred
APPLICANT: Renz, Manfred
APPLICANT: Renz, Manfred
APPLICANT: Renz, Manfred
APPLICANTON: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFERENCE: 8484-0030-999
CURRENT APPLICATION NUMBER: 1050/89/313,832A
CURRENT FILING DATE: 1996-01-12
PRIOR PEDLICANTON NUMBER: PCT/DE96/00444
NUMBER OF SEQ ID NOS: 2
SEQ ID NOS: 2
SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 6328
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Sequence 1, Application US/08913832A
Patent No. 6329517
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; NAME/KEY: CDS
; LOCATION: (1)...(5736)
US-08-913-832A-1
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532 sLeuProGlnArgCysHisGlyValLeuArgArgArgLysAspTrpAsnMetArgLeuGl 552	Qy 5
1195CCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGAGCTGCCCACACTG 1241	Db 11
513 lGlyAlaGlyThrAlaGluAspAlaLysLeuGlnGluProTrpSerCysTyrMetCy 532	
493 uLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCysLeuGluValLeuVa 513	Qy 4:
477 pGlyTyrGlnSerTyrCysThrValCysCysGluGlyArgGluLeuLe 493	
457 yGlyLeuCysGlnSerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAs 477	Qy 4!
1068 GGAGGAGGTGACTGCTGTG 1086	Db 10
pArgCysLe	Qy 4:
1008 CAGCCGTAGTAGCCGCAGCCGCAAGAAACTCCGAACCACTAAAAAAGAAAAAGAAAAGCCGA 1067	Db 100
417 uAspGluGluSerArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGl 437	Qy 4:
76ATCAATAGCTATTCTGTTTCTGATGGTTCCAC 1007	8
397 rGluSerProProProLysArgLeuLysThrAsnSerTyrGlyGlyLysAspArgGlyGl 417	Ωу 39
937	Db 93
377 uGluProArgArgArgGluAsnLysSerArgArgArgThrThrAsnAspSerAlaAlaSe 397	0у з
362 oValValAsnLys	Qy 36
46 TGCCAAGAAGCCT87	œ
hrGlyIleGlu	,e Vo
98 AGGTCCCAATGCTCGGAGGAAGGCCCAAGGGCAGCCCTCGTGTACCTGA 84	J
322 sThrPheSerSerProGlyGluSerLeuGluAspGlnLeuLysProMetLeuGluTr 342	Qy 3;
38 TGCACCACCTCCCCCTGTGGAGGTGCCTATCCGCAAGGCCAAGACCAAGGAGGGCAA 79	7
02 uValSerTvrArgLvsAlaMetTvrHisThrLeuGluLvsAlaArgValArgAlaGlvLv 3	W
202 PHYSHEUVALALAUGUSTYSEUPIESERGIHHISFREASHLEUALAINIEREASHLYSEUE 302 1	
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267 pValGinTrpPheGlyAspGlyLyspheSerGluIleSerAlaAs 282	
gctgccaaaaatcccaagattgctgtctccaagatgatgatgatgttttgggt	
erTrpLysAlaThrSerLy	Ωу 25
535AAGGCCTTCAGCCAGTTTGTCAGACCCCTCAT 566	Db 53
231 yIleGlyAspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetValVa 251	Оу 23
495 CGTGTTCTCAGAGGAGGATTATCGAACCCTCACCAACTAC534	
211 nValAspAlaGluSerArgAspGlyAspSerThrGluTyrGlnAspAspLysGluPheGl 231	0у 21
	Db 45

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE;
; NAME/KEY: CDS
; LOCATION: (1)...(5736)
US-09-249-181A-1
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6328
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APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC
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373 GAGAAGAAGAACAAAT
                        131 uArgGlnArgAlaSerProArgIleThrArgGlyArgGlnGlyArgHisHisValGlnGl 151
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                                                                                                     9ThrArgSerGluSerProAlaValArgThrArgHisSerAsnGlyThrSerSerLeuGl 131
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o d	171	rThrProfrpSerSerProAlaSerValAspPheMetGluGluValThrProLysSerVa 191 ::
ò	191	SerThrProservalAspLeuSerGlnAspGlyAspGlnGluGlyMetAspThrThrGl 21
Q	451	
g g	211	nVaAspAlaGluSerArgAspGlyAspSerThrGluTrGluTAspAspLysGluPhaGl 231
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e 6	251	1Setitplys
ò	267	pValGlnTrpPheGlyAspGlyLysPheSerGlulleSerAlaAs 1::::::
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· 음	738	TGCACCACCACCTCCCCTGTGGAGGTGCCTATCCGCAAGGCCAAGGACCAAGGGGAA 797
ò	322	hrPheSerS
qq	798	AGGTCCCAATGCTCGGAGGAAGCCCAAGGGCAGCCCTCGTGTACCTGA 845
ò i	342	yGlyPhelysProThrGly1leGluGlyLeuLysProAsnLysLysGlnPr
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6 6	362	oValValAsnLysSerLysValArgArgSerAspSerArgAsnLe 377
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& 8	377	uGluProArgArgArgGluAsnLysSerArgArgArgThrThrNanAspSerAlaAlaSe 397
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QQ	916	 ATCAATAGCTATTCTGTTTCTGATGGTTCCAC 1007
ò	417	uAspGluGluSerArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGl 437
qq	1008	CAGCOGTAGTAGCCGCAGCAGGAAGAAACTCCGAACCACTAAAAAGAAAAGAAAAGGGGA 1067
ò	437	uAspArgCysLeuSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGl 457
gg	1068	GGAGGAGGTGACTGCTGTG
ò	457	yGlyLeuCysGlnSerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAs 477
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ò	4	pGlyTyrGlnSerTyrCygThrValCysCQsGluGlyArgGluLeuLe 493
qq	1089	TGGTTATGAGACAGACCACCAGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCAT 1148

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgTyr-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGAACTTGTTCGTATTTTAGAAACAAAAAAACCTCGTGTTGCA------
                               ProValValMetAsnGlyLysAspAspValLeuTrpCysThrGluLeuGlu-----Arg 813
CCTATAATCCTTACATATAGCGGAGATATTCGTAAATTAACACCAAGAGAATGCTTTAAC 2210
                                                                     AGTAATTTAGTACCAACACTAACGGCTAATATGGGAACAGGTGGGCATAAT-----GTG 2150
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                                                                                                                                                                         ----ThrAlaLysLeuLysLysValGlnThrIleThrThrLys 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TCTGAGTTAGAAAGACTA 1799
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US-09-720-086-6 (1-859) x US-08-760-745-4 (1-2376)
                                   Query Match:
                                                               Percent Similarity
                                                                                                   Alignment Scores:
                                                                                                                              US-08-760-745-4
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Patent No. 5972658
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                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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LENGTH: 2376 base pairs
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                    RESULT 6
US-08-962-284-1
| Sequence 1, Application US/08962284
| Patent No. 598608
| GENERAL INFORMATION:
| APPLICANT: Luna, Elizabeth J. |
| APPLICANT: Peoper Kobert K. |
| APPLICANT: Pope, Robert K. |
| APPLICANT: Pope, Robert K. |
| APPLICANT: Pope, ADPLICANT: MILEUNDING POLYPEPTIDES |
| TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THE SAME |
| NUMBER OF SEQUENCES: 3 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Fish & Richardson P.C. |
| STREET: 225 Franklin Street |
| CUTY: Boston |
| CUTY: Boston |
| CUTY: Poston |
| CUTY:
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Matches:
Conservative:
Mismatches:
Indels:
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ZIP: 02110-2804

CMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OFRATING SYSTEM: Windows5
SOFTWARE: PastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,284
FILING DATE: 31-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET UNDABER: 07917/058001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER/STICS:
TURNEY: WINDER: WIN
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; LOCATION: 451...5814
US-08-962-284-1
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144.50
32.24%
20.39%
3.15%
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STRANDEDNESS: double
                                                                        1108 CATGGCCTGCAAA 1120
460 sGlnSerCysArg 464
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MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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300 2266	288 lyLeuPheSerGlnHisPheAsnLeuAlaThrPheAsn	р <i>у</i>
N	 47 AATATGCTGTTCCCAGAAGAGGAAGCCTGGAACGGGCGAACCCTCCCATCACCCACC	N
88	83LysLeuValAlaLeuG	
282 2146	TACCCCATCCTGAACAGAGCCAGGGAAGGAGACAGCCATAAGGAATCTA	2 2
0	48 GAGÀCAGTGGGATGGAGAAGTATGGGTCCTTTGAGGÀAG	2
279	TrpValGlnTrpPheGlyAspGlyLysPheSerGluI	¥
2047	AAGGGAATGTTGAGAGAATATGGAGAGAGAGAAAGCAAGAGAGAG	<u>р</u>
265	ProGlyM	¥
	48CTGAAATCGCAAGCTTGGCAGCCTTTGGTAGAGGGTAGCG	ш
247	spLeuValTrpGlvLvsIleLvsGlvPheSerTrpTrpPro	ξ
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1888		pu pu
	96 AlAsni.anSerGluBsnGlvBsnGlnGlnGlnGlnWarAsnThrFlnValBsnBlaGlnS	
196	78 laSerValAspPheMetGluGluValThrProLysSerValSerThrProSerV ::: % TGAACACA	f &
1795	36 TCACACTGGGAGAGGTGGAGGGTGCAGAGTGGAAAGCTCATTCCTTTCTCACCTGCCG)b 17
178	58 laThrArgSerArgArgArgArgAlaSerSerSerAlaSerThrProTrpSerSerProA	γ 1
158 1735	38 rgIleThrArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProA :::	2y 1 3b 17
1707	67 CGATTTCTACCCGGAACAGAATAGACACGAGACAGAGGAGGAG	
138	8 laValArgThrArgHisSerAsnGlyThrSerSerLeuGluArgGlnArgAlaSerProA	ş
1666	33TTGTTTAACAAATTGTCCCAGCCAGTCTCAAAAG)b 16
	22 AMANG I INDUCT	; ;
, 00	78 lnAspMetThrGlyAspGlyAspArgAspAspGluValAspAspGlyAsnGlySerAspI	
78 1621	59 ArgArgSerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrG	ο _ρ 12
1561		ეხ 15
58	proGluThrArgGly	Ϋ́

luValCysAlaGluSerIleAlaValGlyThrValLysHisGluGly 626	IleAlaSerGluVal	809	Ş Q
ACTGAGCAGAGATTAAACGTTGCCTTCATGGAGTCAAAGCGGATGAAAGTAGAAAAGATG 3366	ACTGAGCAGAGATTA	3307	뫄
euLysGluLeuGlyIleLysValG		595	γQ
AACCCCTGAAAATGCTGGCGGCAAGAGAAGATCTCCTTCAGGAATAC 3306	CAGGCCTCCAAAAACCC	3247	망
ArgProlleArgValLeuSerLeuPheAspGlyIleAlaThrGlyTyr 594	Arg	579	Ş
 CCAAATTGACGTCTTCCGTGGCCGAGCACAAGCGGGCAGTTAGGCCCAAGCGCCCGGGTT 3246		3187	ם
ProAlaIleProAlaAlaLysArg 578	ProLysLeuTyrPro	567	Ş
AGAAGTCCTGTGGAGATGATGAGGACTTCGATGTCATTTTCGATCCTTATGCA 3186	CCAAGAAGTCCT	3130	Вр
ArgLeuGlnAspPhePheThrThrAspProAspLeuGluGluPheGluPro 566	ArgLeuGlnAspPhe	550	Ş
CTTTGCCAAATTTTACCGCAGCGTGGATTATAATATG 31	:::::: ATGAAGCCAGATGATGATGAAAC	7	문
ArgArgLysAspTrpAsnMet 549	LeuArg	541	۶ ک
uProTrpSerCysTyrMetCysLeuProGlnArgCysHisGly-Val	laLysLeuGlnGluP	521	\$ 8
AAGAAGGCTGAATAAC 3009		. 2994	망
ysArgCysPheCysValGluCysLeuGluValLeuValGlyAlaGlyThrAlaGluAspA 521	ysArgCysPheCysV	501	γ
AGACCAGATATGCAGTTAGAATCGGACCTGAAGTTGGACAGGCTGGAAACCTTTCT 2993	AGACCAGATATGCAG	2938	Db
ysCysGluGlyArgGluLeuLeuCysSerAsnThrSerCysC 501	yrCysThrValCysCysGlu	482	Ş
ATTTGCGGTAAAACAAGAGGCACCACACCCGTTTCCAAACCCCTGGAAGATATCGAAGCC 2937	ATTTGCGGTAAAACA	2878	Дb
TyrGlnSerT 482		479	Ş
GAAGAAAGGTTTGGCGTCACCTACTGCCATAACCCCCAGTAGCCTCAGCC 2877	::: GAAGAAA	2829	망
spArgPheLeuGluLeuPheTyrMetTyrAspGluAspGly 478	lnSerCysArgAspA	461	Ş
GGAGCGGCCAACGACTCGACCCAGTTCACTGTGGCTGGCAGGATGGT 2828	GGAGCGGCCAACGAC	2782	당
ysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCysG 461	erCysGlyLysLys-	442	Ş
TIGAGGAGGAAGCAGCTCATCACTGT-GAGAGAGGAGGGCCTGGAAGACGAGAGGCAGA 2781	 TTGAGGAGAGGAAGC	2723	g
gGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCysLeuS 442	rgGluArgMetAlaS	422	Ş
ACAGAAAGTCGAGAGAGCCAAATGACGA 2722	AGAAGCGGGTC	2684	Вb
roLysArgLeuLysThrAsnSerTyrGlyGlyLysAspArgGlyGluAspGluGluSerA 422	roLysArgLeuLysT	402	φ
AGGGCGGCAAGGCCGGCCAGCAGCCTGCACACCCAGGAAGCAGGGCGGTCCCTCATCA 2683	AGGGCGGCAAGGCGC	2624	В
-AsnLysSerArgArgArgThrThrAsnAspSerAlaAlaSerGluSerProProP 402	luAsnLysSerA	383	γQ
TGGCACTGTTGAAGAAAAGCGGGGAGGAAGATTGGAGAAACAGACTCAGCAGGAGGCAGG 2623	TGGCACTGTTGAAGA	2564	В
erLysValArgArgSerAspSerArgAsnLeuGluProArgArgArgG 383	alValAsnLysSerL	363	Q V
GAGGGCCTTCTTGACTCACCCAGCAAAACCATGTCTATTAAAGAAAG	CGACAGGGGAGGGCCTTC	2507	D
luGlyLeuLysProAsnLysLysGlnProV 363	roThrGlyIleGluG	349	ρ
ACG	; ; ; CACAGGAGAAGCTCT	2447	Дb
ProMetLeuGluTrpAlaHisGlyGlyPheLysP 349	lnLeuLys	335	Ş.
	AAACTATTGCTCAAA	2387	당 \$
Para	CHARACTARACTAR	202	Ş

U.S.A.

COUNTRY:

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3367 TCTTCCAACTCCAACTTCTGGAAAGTCACCCTGGCGGGTTTAGCCAGTAAAGAAAACTTC 3426
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                                                                                           3427 AGCAACGTCAGCCTGCGGAGCGTCAAC------CTGACGGAACAGAACTCTAAC 3474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3676 TTAATTCAGACAAAGAGGGAACTTGGTTGTAGAGCTACTTATATCCAAACCATTGAAGAA 3735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3970 GGTAGTGAAGTT-----TACGTATGGCATGGAAAGAAGTCACATTAGCACAA 4017
                                                                                                                                                                                                                                                                                                                               679 PheGluPheTyrHisLeuLeuAsnTyrThrArgProLysGluGlyAspAsnArgProPhe 698
                                                            627 ------GlnIleLysTyrValAsnAspValArgLysIleThrLysLysAsnIleGlu 643
                                                                                                                                                  644 GluTrpGly---ProPheAsp-----LeuVallleGlyGlySerProCysAsn 658
                                                                                                                                                                                                                                         659 AspLeuSerAsnValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhe 678
                                                                                                                                                                                                                                                                                                                                                                                                                  699 PheTrpMet-----PheGluAsnValval------AlaMetLysValAsnAsp 712
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APPLICANT: Crupper, Scott S.
TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Boulevard, Suite 400
CITY: Kanas City
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08931999
Patent No. 6043219
GENERAL INFORMATION:
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US-08-931-999-4
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4542 -----ACGGAAGAAAA---ACACCCCGAAAAAACAACAAAAAGACAACAACAAAAAACA 4592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 LysLeuThrArgGluThrLysAspThrArgThrArgSer--GluSerProAlaValArgT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 ------AspArgAspAspGluValAspAspGlyAsnGlySerAspIleLeuMetPro 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 SerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAspMetThrGlyAspGly--- 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 AsnPheSerAspGlnSerSerAspThrLysAspAlaProSerProProValLeuGluAla 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 IleCysThrGluProValCysThrProGluThrArgGlyArgArgSerSerArgLeu 65
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,999
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-720-086-6 (1-859) x US-08-931-999-4 (1-6755)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710,561
FILING DATE: 19-SEP-1996
ATOMNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
                                                                                                                                                                                                                                                                                             TELEPHONE: 816/474-9050
TELEPHONE: 816/474-9050
TELEPHONE: 816/474-9050
TELEPHONE: 816/474-9050
INFORMATION FOR EEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6755 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIT-SENSE: NO
TIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
STRAIN: UT0007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
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132.50
35.018
19.908
2.898
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STRANDEDNESS: double
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Best Local Similarity:
                                                                                                                                             FILING DATE:
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ANTI-SENSE: N
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                                                                APPLICANT: Hadary, Dany
APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
TITLE OF INVENTION: STREPTOMYCES
TITLE OF INVENTION: STREPTOMYCES
TITLE OF INVENTION: POLYPEPTIDES
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                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & I
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                                                                                                                                                                                                          INFORMATION:
3: Foley & Lardner
                                                                                                                                                                     Butler, Michael J.
                                                                                                                                                                                       Bartfeld,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGAMAAAAGAGAAAAAGGGACAGGGGGGAGGGGCAGAAGGAAACGCCCAAA
                                                                                                                                                                                       Daniel
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                                                                                   PROTEASES AND IMPROVED STRAINS FOR EXPRESSION
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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1874
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: USA
COUNTRY: USA
COUNTRY: USA
CTD: 20007-5109
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LENGTH: 1820 base pair
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APPLICATION NUMBER: US,
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139 eThrArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaTh :::||
                                                                                                                                                                                                                                            246
                                                 414 GCGACGTCCGGCTCGCGGTGGCCCGCAAGAAGGCCACGGGGCCGGGCAAGCGCCTCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
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EDNESS: double
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Krieger, Timothy
APPLICANT: Malek, Lawrence T.
APPLICANT: Malek, Lawrence T.
APPLICANT: Malcx/k. Eva
APPLICANT: Walcz/k. Eva
APPLICANT: Walcz/k. Eva
APPLICANT: Krygsman, Phyllis
APPLICANT: Scarer, Shelia
APPLICANT: Scarer, Shelia
APPLICANT: Scarer, No. Pertipes AND
ITILE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
NUMBER OF SEQUENCES: 2
ADDRESSER: Roley & Lardner
STREET: 3000 K Street, N.W.
                             1354 CGCCTTCTCCCCCCGGACGAGGTGCGCGACGCCCTCCCCGACTTCGAGAAGGCGTCCCC 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1414 GÉTÉTTGGCGAGGCCTCGCCTGGTCCTCCTGAACTGCGCGTACTGGCCGGTGAAGCC 1473
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501 sArgCysPheCysValGluCysLeuGluValLeuValGlyAlaGlyThrAlaGluAspAl 521
                                                                                             521 aLysLeuGlnGluProTrpSerCysTyrMetCysLeuPro-----GlnArgCysHisGl 539
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ZIP:
ZOUGN-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPA:
COMPUTER: IBM PC COMPA:
SOFTWARE: PATENTIN BATS:
APPLICATION NUMBER: US/08/265,310
FILING DATE: 24-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/173,508
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A:
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08265310; Patent No. 5856166; GENERAL INFORMATION:
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APPLICANT: Butler, Michael J.
APPLICANT: Hadary, Dany
APPLICANT: Jenish, David
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US-08-265-310-7
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US-08-265-310-7
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEFAX: 204136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                  197
                                                                                                                                                                                                                                                                                             354 TCCCGGGCTTCCAGTGCGCCACCATGAAGGCCCCGCTCGACTACGCCAAGCCCGCCGACG 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 CCGGCGCGACGGACGCCACGGCGACCCTGACCCCCTGCCGAA-----GGCCACGC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 GCACCGGCGCACCCGTTTCCGGGCCACGCTGCTCACCGCCGCGCGCTGCTCGCCACCGCCT
216 rArgAspGlyAspSerThrGluTyrGlnAspAsp-----LysGluPheGlyIleGly-- 233
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 AlaProSerProProValLeuGluAlaIleCysThrGluProValCysThrPro-GluTh
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STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 rAspileLeuMetProLysLeuThrArgGluThrLysAspThrArgThrArgSerGluSe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 rThrGlnAspMetThrGlyAspGlyAspArgAspAspGluValAspAspGlyAsnGlySe 96
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                                CCCGTCGAGTGCCTG-GACGGGCGCGAGATGGACGCGTACACGCGCACCGACGTCACCCC 672
                                                              pLeuSerGlnAspGlyAspGlnGluGlyMetAspThr---ThrGlnValAspAlaGluSe 216
                                                                                                                               oAlaSerValAspPheMetGluGluValThrProLysSerValSerThrProSerValAs 197
                                                                                                                                                               GCGGGCATCGGCTACCCGGCGAAGGTCCGCGCCCAGTACGACATGGTGGCGGTCGACCCC 592
                                                                                                                                                                                              rArgSerArgArgArgAlaSerSerSerAlaSerThrProTrp-----SerSerPr 177
                                                                                                                                                                                                                              CGCTGCTGGTCAACCCGGGGAC-CGGGCGGCTCGGCGATCGGCTACCTCCAGCAGTAC 532
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559 oAspLeuGluGluPheGluProProLysLeuTyrProAlaIleProAlaAlaLysArgAr 579	1414 GGTCTTCGGCGAGGGCCTCGCCTGGTCCTCCCTGAACTGCGCGTACTGGCCGGTGAAGCC 1473	539 yValLeuArgArgArgLysAspTrpAsnMetArgLeuGlnAspPhePheThrThrAspPr 559	GGCCTTCTCCTCCCGGACGAGGTGCGCGACGACGCCCCCGACTTCGAGAAGGCGTCCCC	521 aLvsLeuGlnGluProTrpSerCvsTvrMetCvsLeuProGlnArgCvsHisGl 539	501 sArgCysPheCysValGluCysLeuGluValLeuValGlyAlaGlyThrAlaGluAspAl 521		481 rTyrCysThrValCysCysGluGlyArgGluLeuLeuCysSerAsnThrSerCysCy 501	1264 CTCCGACAGCTACTACGAGCGCGACGGC 1297	461 nSerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAspGlyTyrGlnSe 481	1247	ייטייטייטן יין ייטן ייטי פראמיטן פראמיטן ייטיטייטן פראמיטן ייטן ייטן ייטן ייטן ייטן ייטן ייטן	421 rArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCysLe 441	1160 ACCGGCGTG-ATCGCCGCGATGTACGACGAGGCGCCCTGGCAGCAGCT 1206	erTyrGlyGly	1101 CGAAGCCCCTGCCCGCCGACGACGCCG-ACGGCCGCAAGCTCACCGAATCCCTCGCCACC 1159	381 gArgGluAsnLysSerArgArgArgThrThrAsnAspSerAlaAlaSerGluSerProPr 401	361 nProValValAsnLysSerLysValArgArgSerAspSerArgAsnLeuGluProArgAr 381	1029 CCCTCGGCGACAAGGACCACCCCCGACCAGGTCGGCAAGA 1070	hrGlyIleGluGlyLe	970 GGGCTTCGAGACGGCGTTCCAGTCCTTCGCGAAGGACTGCGTGAAGCAGCCGGA-CTGCC 1028	324PheSerSerSerProGlyGluSerLeuGluAspGlnLeuLysProMetLeuGl 341	CTTGGACGGCGATGGACCCCTCGCTGCCGCCCGCCTGAACCTGGAGCAGACGGA	08AlaMetTvrHisThrLeuGluLvgAlaArgValArgAlaGlvLvsThr	291 TGITHISFREASHLANDINFREASHLÝSHEUVALSETTYTATGYS30/	14 GGGCGACGAGAAGCTGACCTACGTGGGAGCGTCGTACGGCACCTTCCTGGGC	271 eGlyAspGlyLysPheSerGluIleSerAlaAspLysLeuValAlaLeuGlyLeuPheSe 291	760 CCACGTCTCCACGGTCGAGGCGGCACGCGACATGGACGTCCTGCGCGCGGTGCT 813	251 lSerTrpLysAlaThrSerLysArgGlnAlaMetProGlyMetArgTrpValGlnTrpPh 271	733 CGGGGCGGACGCG	234AspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetValVa 251	673 GGACGACGCGGCGACACCGACGCCTACAAGGAGTTCGCCGAGGCTG 732

JAME/KEY: mat_peptide Jocation: 2451720 US-08-951-742-7 Alignment Scores:		300 CCGCCGAGCTGCCCGTACTACGAGCAGAAGCTCGGCTGGGCGACTGCGGCG 116 rProalavalargThrArgHisSerAsnGlyThrSerSerLeuGluArgGlnArg 354 TCCGGGCTTCCAGTGCGCCACATGAAGGCCCGGTTCAGCCCAGCGGCGACG 135	Oy 159 krysserArgArgArgArgArlaSerSerSerAlaSerThrProTrpSerSerPr 177	Oy 234AspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetValVa 251 Db 733 CGGGGGAGCGC
Db 1474 CACGGGGAGCCGCACCGC		Dan BENZ	ZIP: 20007-5109; COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM FC compatible COMPUTER: TBM FC COMPATIBLE COMPUTER: TBM FC COMPATIBLE COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/88/951,742 FILING DATE: 16-CCT-1997 ATTORNEY/AGENT INFORMATION: NAME: Bent, Stephen A: REFERENCE/DOCKET NUMBER: 0189740/0140 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 1NFORMATION: TELECOMMUNICATION 1NFORMATION: TELECOMMUNICATION 1NFORMATION: TELECOMMUNICATION 1NFORMATION:	O O C 4 O M G

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CACCGCCCCGGAGGACGCCAAG 1711
                                                                                             uLysTyrIleAlaSerGluValCysAlaGluSer------IleAlaValGl
                                                                                                                              CCTCTCCGACCAGCTCACCTCCGGCCACCTCCTCACCTACGAG---GGAGACGGCCACAC
                                                                                                                                                            rLeuPheAspGlyIleAlaThrGlyTyrLeuValLeuLysGluLeuGlyIleLysValGl
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                                                                                                                                                                                                                               gProIleArgValLeu-----Se 585
                                                                                                                                                                                                                                                                                                oAspLeuGluGluPheGluProProLysLeuTyrProAlaIleProAlaAlaLysArgAr 579
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                             YThrValLysHisGluGlyGln 627
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RESULT 11
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SCOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-973-675-1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,675
FILING DATE: 12-DEC-1997
CLASSIFICATION: 1435
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICANT: HATEBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ADENOVIRUS TITLE OF INVENTION: INHIBITOR C
                                                    972 CACCAGAGGGCCTGGATTCCTTCTGAAAACATTCAAGATATCACAGTCAACATTCATCGG
                                                                                                                                                                                                                            254 LysAlaThrSerLysArgGlnAlaMetProGlyMetArgTrpValGlnTrpPheGlyAsp
                                                                                                                                                                                                                                                                                               234 AspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetValValSerTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
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----LysLeuValSerTyrArgLysAlaMetTyrHis---ThrLeuGluLys
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Matches:
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Mismatches:
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212 GCAAAG------AAAGGACGACGTAATCAAAGTGTGGAGCCAAAAG 1253
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1032 CTGCACGTGAAGCGCAGTATGGGTTGGAAAAAGGCCTGTGATGAGCTGGAGCTGCATCAG 1091
                                                                                  1092 CGTTTCCTACGAGAAGGGAGATTTTGGAAATCTAAGAATGAGGACCGAGGTGAGGAAGAG 1151
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                                        316 AlaArgValArgAlaGlyLys----- 322
                                                                                                                             323 -----ThrPheSerSerProGlyGluSerLeuGluAspGlnLeuLysProMet 339
                                                                                                                                                                                                               340 LeuGluTrpAlaHisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnLys 359
                                                                                                                                                                                                                                                                                                  360 LysGlnProValValAsnLysSerLysValArgArgSerAspSerArgAsnLeuGluPro 379
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TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
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1740 ATGTACCACTGCTGCTGGAACAATCCTACTGCTCCATCAAGTGC 1784
                                                                                                                                                                                                                                                                                                                                                                                         ArgArgArgGluAsnLysSer------
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COUNTRY: US
ZIP: 53701-2113
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31409 CAAGAAGATGTTTCTTTACTAAATGCAGAAATAATTAAGGGTTTTTTTAAAAACGATATG 31350
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31244 TTAGTATCA------GAATTACAGCCATTATTCTTTTTGGCAGAA 31206
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dc-1999
CLASSIFICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seav, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEFAX: (608) 251-9166
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Mismatches:
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; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-453-702B-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: 96
SEQUENCE CHARACTERISTICS
COMPUTER READABLE FORM
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40.69%
25.11%
2.73%
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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                                                                    Db 1606162 GTCCGTTCATGCCGTGCGCAC------
                                                                                                                                                 Db 1606102 CTGCCGCTGGATGGCACCGGCGGTGCTCCGCGCCAAACAATAGTGTCTCGGTAACCGCCG 1606161
                                                                                                                                                                                                                                  Db 1606042 ATGCGGACAGAATCTCGACGATCCCGATGCCGCGTTTCGGGTGCAGATGGCGCTGGAGGT 1606101
                                                                                                                                                                                                                                                                                                                      Db 1606027 CCAGGCGATGGAACT----- 1606041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 1605907 CGACGAGCGCAATAGCTGGCTACGCGAGACGTTACGGGAGTTCTTGCTGCGTAACCGCAG 1605966
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31010 ATGCCTAAAATGATTGATCCGGTTACTGTAAAA 30978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31055 GGTGTAAAAAATCATTGAAGCTTGATATTTCAGAT----
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                                                                                                       142 GlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaThrArgSer 161
                                                                                                                                                                                    125 -----AsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThrArg 141
                                                                                                                                                                                                                                                                 112 ThrArgSerGluSerProAlaValArgThrArgHisSer------
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162 ArgArgArgArgAlaSerSerSerAlaSerThrProTrpSerSerProAlaSerValAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  773 LysLeuLysLysValGlnThrIleThrThrLys 783
                                                                                                                                                                                                                                                                                                                                                80 MetThrGlyAspGlyAspAspAspAspGluVal-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 ArgSerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAsp 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-086-6 (1-859) x US-09-103-840A-1 (1-4411529)
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p. 6294328
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125.50
30.39%
21.85%
2.73%
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Matches:
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61
245
258
                                                             -----AATCGTGGT 1606191
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Qy 458 GlyLeuCysGlnSerCys
Qy 439 ArgCysLeuSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGly 457
Oy 419 GluGluSerArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAsp 438
Qy 402ProlysArgLeuLysThrAsnSerTyrGlyGlyLysAspArgGlyGluAsp 418
Qy 394 SerAlaAlaSerGluSerProPro
Qy 376 AsnLeuGluProArgArgArgGluAsnLysSerArgArgArgThrThrAsnAsp 393
QY 366
354GlyLeuLysProAsnLysLysGlnProValValAsn
Qy 339 MetLeuGluTrpAlaHisGlyGlyPheLysProThrGlyIleGlu 353
Qy 319 ArgAlaGlyLysThrPheSerSerSerProGlyGluSerLeuGluAspGlnLeuLysPro 338
Qy 299 PheAsnLysLeuValSerTyrArgLysAlaMetTyrHisThrLeuGluLysAlaArgVal 318
Qy 288 GlyLeuPheSerGlnHisPheAsnLeuAlaThr
Qy 270TrpPheGlyAspGlyLysPheSerGluIleSerAlaAspLysLeuValAlaLeu 287
Qy 253 TrpLysAlaThrSerLysArgGlnAlaMetProGlyMetArgTrpValGln 269
Oy 241LysGlyPheSerTrpTrpProAlaMetValValSer 252 ::
Qy 222 ThrGluTyrGlnAspAspLysGluPheGlyIleGlyAspLeuValTrpGlyLysIle 240 b 1606340
Oy 202 GlyAspGlnGluGlyMetAspThrThrGlnValAspAlaGluSerArgAspGlyAspSer 221
Qy 182 PheMetGluGluValThrProLysSerValSerThrProSerValAspLeuSerGlnAsp 201
Db 1606192 CGTGAGCTTCGGTGTCGGCGCATATGGTCTCCGACGGATTCGGCGCCT 1606239

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Oy 493 ---LeuleuCygSerAsnThrSerCygCygArgCygPheCygValGluCygLeuGluVal 511
bb 1607369 CCTATATTCTGCTTCCCAACGAGGATCTGCCGTTGC--TGCAGCCGCTGCGTTG 1607425
                                                      Db 1607190 CATTTACACGACCAATACGACGCTTTGCCGACTTCCCGAAGTACCCGCTCAACATCCT 1607249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1607489 -------ACCGAACCGGATACGCCGATGTTCCGACCCCGCCCCA-CTGTTC 1607532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 1607593 CTCACCGCCCTG------GATGCCTTGCTCGACACCGTGATCAACGATCAAT 1607643
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472 TyrmetTyrAsp------475
                                                                                                                     476 -----GluAspGlyTyrGlnSerTyrCysThrValCysCysGluGly--- 489
                                                                                                                                                                                                                                                     490 -----ArgGluLeu----- 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 CysLeuProGlnArgCysHisGlyValLeuArgArgArgLysAspTrpAsnMetArgLeu 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 -----IleAlaThrGly---TyrLeuValLeuLysGluLeuGlyIleLysValGluLys 606
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COMPUTER: IBM PC_Compatible ...
CORFIAING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ENHANCED EXPRESSION OF TITLE OF INVENTION: PROTECLYTIC ENZYMES IN KOJI MOLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oy 607 TyrileAlaSerGluValCysAlaGluSerileAlaValGly 620
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Patent No. 6090607
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MOLECULE TYPE: DNA (genomic)
FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
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LENGTH: 4657 base pair:
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LOCATION: 1189..1604
FEATURE:
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US-09-254-325-1
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2398 ACGGATTICTICTCTCCACCGCCATCAGGCTACCAGGCCATCC----- 2445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 AspGlyAspSerThrGluTyrGlnAspAspLysGluPheGlyIleGlyAspLeuValTrp 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 GluProValCysThrProGluThrArgGlyArgArgSerSerSerArgLeuSerLysArg 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AsnGluGluGluGluGlyAlaSerGlyTyrGluGluCysIleIleValAsnGlyAsnPheSer 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 AspGlnSerSerAspThrLysAspAlaProSerProProValLeuGluAlaIleCysThr 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 GluValSerSerLeuLeuAsnTyrThrGlnAspMetThrGlyAspGlyAspArgAspAsp 88
                                                                                                                                                               OTHER INFORMATION: /label= TRUNCATED-AREA
OTHER INFORMATION: /note = "AREA IS TRUNCATED IMMEDIATELY
OTHER INFORMATION: DOWNSTREAM THE SEQUENCE ENCODING
OTHER INFORMATION: A DNA BINDING DOWAIN"
                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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Matches:
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125.00
30.56%
20.04%
2.72%
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                                                                                                                                            OTHER INFORMATION: /1
OTHER INFORMATION: /n
OTHER INFORMATION: /n
                                                                                 1704..3846
                       1605..1703
                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                exon
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                       NAME/KEY:
LOCATION:
                                                                                 LOCATION:
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DB:
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; Sequence 5, Application US/09079415
; Patent No. 6013452
; GENERAL INFORMATION:
APPLICANT: Christensen, Tove
; APPLICANT: Lehmbeck, Jan
TITLE OF INVENTION: A Fungus Wherein Th
; TITLE OF INVENTION: pepE Genes Have Bee
; NUMBER OF SEQUENCES: 12
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US-09-079-415-5
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COMPUTER READABLE FORM:
                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60134520 No. 6013452disk
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                  ZIP:
                                                 CITY: New York
STATE: NY
                                                                                  STREET:
                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      PheLeuGluLeu
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                                                                                                                                                                                                                                                                                                                                                                                                         CCA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACGGCGAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgGlyGluAspGluGluSerArgGluArgMetAlaSerGluValThrAsnAsnLysGly 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCGAGTCCGCCCTGAGCAGCGCAGTTCCGTCCCGCCCAGTCCCGGGGGGCAGCAAG 3207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTTGCGCCAAAGCATGCACTCTAATAACAATACGTCTCATACCTCCCCTAATACGCCG 3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCAGGACCCTCGCCGGCAGAAGATTGCGCGCGCACCACGTCCACCCCCAATACGGCCCAG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnLeuGluProArgArgArgGlu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProMetLeuGluTrpAlaHisGlyGlyPhe-----LysProThrGlyIleGluGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValArgAlaGlyLysThrPheSerSerSerProGlyGluSerLeuGluAspGlnLeuLys 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTTCCATTCGCTGCCGGGCTTTGGCCCTCAA------CATCGCAAGCAT 2916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrPheAsnLysLeuValSerTyrArgLysAlaMetTyrHisThrLeuGluLysAlaArg 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluIleSerAlaAspLysLeuValAlaLeuGlyLeuPheSerGlnHisPheAsnLeuAla 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysArgGlnAlaMetProGlyMetArgTrpValGlnTrpPheGlyAspGlyLysPheSer 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GACGGGTTCTCG---
                                                                                                                                                                                                                                                                                                                                    TTTTTGAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                     ProValSerPheHisProLeuPheGluGly---GlyLeuCysGlnSerCysArgAspArg 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnLeuGluAspArgCysLeuSerCys------
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                  10174
                                                                                   405 Lexington Avenue
                                  USA
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                                                                                                    6013452th America,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5643 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Rozek, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
 3662 TCGCTGCAG--
                                                                                                                                                                                                                                                                                                                                                                                                     3419 AGCGAGTCTCCGATGGCCTCCGGTCATCCG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                3581 TATTTCGATATGCCGTCGGGC-
                                                                                                                                                                                                                                                                   3497 ACGGATTTCTTCTCCACCGCCATCAGGCTACCAGTCCACGGCATCC----
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LOCATION:
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                                                                                                                                                              89 GluValAspAspGlyAsnGlySerAspIleLeuMetProLysLeuThrArgGluThrLys 108
                                                                                                                                                                                                                                                                                              49 GluProValCysThrProGluThrArgGlyArgArgSerSerArgLeuSerLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Aspergillus
STRAIN: IFO4177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                  29 AspGlnSerSerAspThrLysAspAlaProSerProProValLeuGluAlaIleCysThr 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 5643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AsnGluGluGluGlyAlaSerGlyTyrGluGluCysIleIleValAsnGlyAsnPheSer
                                                                                                                                                                                                                         GluValSerSerLeuLeuAsnTyrThrGlnAspMetThrGlyAspGlyAspArgAspAsp
                           SerLeuGluArgGlnArgAlaSerProArgIleThrArgGlyArgGlnGlyArgHisHis 148
                                                                GACGCGCGCACCCAGCGCCGCATTCCGAACTATATTTCGCATCGGTCCAACTTGTCTGCT
                                                                                                                                                                                                                                                                                                                                     AACCTCTATTCGCATACC---------CCGGTGGCTTCGTCCCTCAACTCG
                                                                                             AspThrArgThrArgSerGluSerProAlaValArgThrArgHisSerAsnGlyThrSer 128
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join(2282..2700,
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2701..2769
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Matches:
Conservative:
Mismatches:
Indels:
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Db 4421 TTTTTGAAATTG 4432 Search completed: November 25, 2002, 02:56:29 Job time : 4354.34 secs

7808 7808 7808

158.5 158.5 158.5 157 157 156.5 156.5

2680 9551 9551 20235 20235 20235 1736 17808 1681 5468 5471

Mon Nov 25 08:18:36 2002

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CURRENT APPLICATION NUMBER: US/09/276.511

PILLING DATE: Herewith CLASSITETICS FLAND CLASSITEMENT APPLICATION DATA:

PILLING DATE: Herewith CLASSITETICS FLAND CLASSITETICS FOR APPLICATION NUMBER: US/09/276.511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLICANT: Buegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 313 174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-676-967-5
US-09-098-487-5
US-09-98-487-5
US-09-98-487-5
US-07-945-283-1
US-08-056-200-93
US-08-056-200-93
US-08-149-097D-22
US-08-149-097D-22
US-09-535-008-66
US-09-535-008-66
US-09-535-008-74
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Sequence 4, Appl
Sequence 1, Appli
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Best Local Similarity:
Query Match:
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REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555;
TELEPAX: (650) 845-4166;
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
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                                                                                                         GluTyrPheAlaCys 911
                                                                                                                                                                                                  ArgLeuLeuGlyArgSerTrpSerValProVallleArgHisLeuPheAlaProLeuLys
                                                                                                                                                                                                                                                                                                      GACTACTTTGCATGT 611
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                                                                                                                                                                               AAGCTGCTGGGAAGGTCCTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGG---CGGCTCTTCTTCGAATTTTC-CACCTGCTGAATTACTCACGCCCAAGGAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspAspArgProPhePheTrpLeuPheGluAsnValValAlaMetGlyValSerAspLys 766
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RESULT 1 US-09-276-531-47

Sequence 47, Application US/09276531 Patent No. 6183968 GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hilfman, Jennif
PPLICANT: Yue, Henry
PLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J

Lal, Preeti Hilman, Jennifer

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COUNTRY: USA
ZIP: 94304
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy d:

STREET: 3174 PORTI CITY: PALO ALTO STATE: CALIFORNIA

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,(
PILING DATE: MATCh 27, 1998
CLASSIFICATION:

60/079,677

596

536 988 476 866 416 846 826 296 806

356

ATTORNEY/AGENT INFORMATION:

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5576 13842 36778 38506 38506 5467 11907

5480 5564 5567 5573

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ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
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ORGANISM
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AUTHORS
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JOURNAL
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Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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Direct Submission
Submitted (28-MAY-1998) CVRC,
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Nat. Genet. 19 (3), 219-220 (1998)
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Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13t
Charlestown, MA 02129, USA
Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327977.
Location/Qualifiers
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Okano, M., Xie, S. and Li, E.
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                                                                1094
                                                                      Eutheria;
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Accession Numbers AA052791, AA111043, AA154890, AA240794,
AA756653, W58898, W59299, W91664, and W91665"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                             /gene="Dnmt3a"
/function="de novo DNA methylation"
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   3.25e-211
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Sciurognathi; Muridae; Murinae; Mus
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341	etProLeuSerSerPheCvsSerAlaPheHisGlnAlaThrTvrAsnLvsGlnProMet	90
37	GCTCCTTCTGCAGTGCATTCCACCAGGCCACCTACAACAAGCAGCCCATG 1	
361 1297	TyrArgLysAlaileTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPhe 3	80 356
381	ProAlaCysHisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnLys 4	00
401	GlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluPro 4:	20 476
1477	ProGluGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGlu 4.	40 536
441	AlaAlaAlaTyrAlaProProProProAlaLysLysProArgLysSerThrThrGluLys 4	60 . 596
461 1597	ProLysValLysGluIleIleAspGluArgThrArgGluArgLeuValTyrGluValArg 4:	80 656
491 1657	GlnLysCysArgAsnIleGluAspIleCysIleSerCysGlySerLeuAsnValThrLeu 5	00 716
501	GluHisDroLeuPheIleGlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGluCys 5	20 776
521 1777	AlaTyrGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrIleCysCysGlyGlyArg 5	40 836
541 1837	GluvalleumetcysGlyAsnAsnAsnCysCysArgCysPheCysValGluCysValAsp 5	896
1897	LeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCysTyr 5	956
581 1957	MetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrpProSerArg 6	016
601	LeuGlnMetPhePheAlaAsnAsnHisAspGlnGluPheAspProProLysValTyrPro 6:	20 076
621 2077	ProvalproalaGluLysArgLysProIleArgValLeuSerLeuPheAspGlyIleAla 6.	40 136
641 2137	YIleGlnValAspArgTYrIleAlaSerGlu 6 	60 196
661 2197	ValCysGluAspSerIleThrValGlyMetValArgHisGlnGlyLysIleMetTyrVal 6	80 256
681 2257	GlyAspValArgSerValThrGlnLy8HisIleGlnGluTrpGlyProPheAspLeuVal 7	00 316

RESULT 2

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RESUL AAT218

AAT21884 standard; cDNA to mRNA; 301 BP. ID

AAT21884:

AC XX

14-AUG-1996 (first entry)



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Human gene signature HUMGS03426.
           Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
XX
KW
ХX
            Homo sapiens.
os
            WO9514772-A1.
 PN
            01-JUN-1995.
                                               94WO-JP01916.
             11-NOV-1994;
 PF
                                               93JP-0355504.
            12-NOV-1993;
 PR
 XX
             (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
  PA
  ХX
             Matsubara K, Okubo K;
  XX
             WPI; 1995-206931/27.
  DR
             Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
  XX
PT
  PT
  PT
PT
  XX
              Claim 1; Page 991-992; 2245pp; Japanese.
             A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) from various human tissues; synthesis of cDNA was initiated from the from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
  CC
CC
               Sequence 301 BP; 96 A; 65 C; 63 G; 66 T; 11 other;
                                                           6.6%; Score 285.2; DB 16; Length 301;
95.3%; Pred. No. 1.5e-48;
vative 0; Mismatches 14; Indels 0;
         Best Local Similarity 95.
Matches 287; Conservative
                                                                                                                                                            0;
                           GATCAGATAGGAGCACAAGCAGGGGACGGAAAGAGAGACACTCAGGCGGCAGCATTCC 3578
    Qy
     Db
                            Qу
      Db
                            Qy
      Db
                             CCACACAGGAAACCTTGAAGAAAATCAGTTTCTAGAAGCCGCTGTTACCTCTTGTTTACA 3758
      Oy
       ВÞ
                            GTTTATATATATATGATAGATATGAGATATATATATAAAAGGTACTGTTAACTACTGTAC 3818
       Qy
                  3759
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3819 A 3819 301 À 301

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool/US09720086/runat 18112002_092832_22195/app_query.fasta_1.4252
-Q=/cgn2 1/USPTO_spool/US09720086/runat 18112002_092832_22195/app_query.fasta_1.4252
-DB=GenEmbl -QFMT=fastap -SUFFIX=ye -MIMMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US09720086_@CGN 1 111308_@runat 18112002_092832_22195 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
   US-09-720-086-5
4909
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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                                                                                                                                                                                                         Journal 10, 1921

Xie, S., Okano, M., and Li, E.

Xie, S., Okano, M., and Li, E.

Submitted (128-MAY-1998) CVRC, Mass. Gen. Hospital, 149 13th Street,

Charlestown, MA 02129, USA

3 (basse I to 4192)

Okano, M., Chijiwa, T., Sasaki, H. and Li, E.

Okano, M., Chijiwa, T., Sasaki, H. and Li, E.

Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,

Charlestown, MA 02129, USA

Sequence update by submitter

Sequence update by submitter

On Nov 18, 1999 this sequence version replaced gi:3327977.
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Ckano, M., Xie, S. and Li, E.
Cloning and characterization of a family of novel mammalian DNA (cyroaine-5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
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/db xref="GI:649468"
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/note="contains Cys-rich region"
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Submitted (01-MAY-2001) National Institutes of Health, Mammalian Submitted (01-MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, MD 20892-2590, tnstitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mus musci
NIHAMGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Meb site: http://www-shgc.stanford.edu
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                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consertium/LMLML at: http://image.llnl.gov Series: IRAK plate: 8 Row: n Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6681208.
Location/Qualifiers

1. 4094
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Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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Direct Submission
Submitted (12-FEB-2001) CVRC, Mass. Gene
Street, Charlestown, MA 02129, USA
Sequence update by submitter
On Feb 12, 2001 this sequence version re
Location/Qualifiers
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Cloning, expression and chromosome locations gene family
Gene 236 (1), 87-95 (1999)
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Direct Submitsion
Submitted (25-MAY-1998) CVRC, Mass.
Street, Charlestown, MA 02129, USA
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Xie,S., Wang,Z., Okano,M., Nogami,M., Li,Y., He,W.W.
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/function="de novo
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PGMNRPLASTYNDKLELOBCLEHGRIAKFSKYRTITTRGNSIKGKDQHFPVFWNBKE
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qq	959	CCTCCTGCTGTGCAGCAGCCACTGACCCCCATTCCCCCACTGTGGCTACCACGCCTGAG	1018
ò	260	ProvalGlyGlyAspAlaGlyAspLyaAsnAlaThrLyaAlaAlaAspAspGluProGlu 2	279
셤	1019	CCCGGGGTCCGATGCTGGGGACAGAATGCCACCAAAGCAGGCGATGACGAGCCAGAG	1078
è d	280	280 TyrgluAspGlyArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLeuArgGlyPhe 299	299
ò	300	SerTrpTrpProGlyArg11eValSerTrpTrpMetThrGlyArgSerArgAlaAlaGlu	319
අ (1139	TCCTGGTGGCCCCCATTGTGTCTTGGTGGATGACGGGCCGGAGCCGAGCAGCTGAA 1	1198
රු සි	320 1199	YTHTAKETEVALMETTEPPAGIYARROLVARPHESEVAIVALCEGAGIULOS 	339 1258
ò	340	LeuMet ProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnPro	529
qq	1259	CTGATGCCGCTGAGCTCGTTTTGCAGTGCGTTCCACCAGGCCACGTACAACAAGCAGCCC	1318
ò	360	MetTyrkrglysalaileTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeu	379
qn .	1319	AIGIACCGCAAAGCCAICIACGAAGICCIGCAGGIGGCCAGCCGCGCGGGGAAGCIG 1	1378
g 8	380	Pherroalizeranderrappduserapperdiylyaaliaydiyuaddinasn 3 	399 1438
ò	400	LysGlnMet1leGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGlu 4	119
a	1439		1498
ò	420	ProbroGluGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluPro	139
g	1499	ccaccagaagaagaagaatccctacaaagaagtgtacacggacatgtgggggggg	1558
ò i	440	3luAlaAlaAlaTyrAlaProProProProAlaLysLysProArgLysSerThrThrGlu 4	651
8	1559	3AGGCAGCTGCCTACGCACCTCCACCAGCCAAAAAGCCCCGGAAGAGCACAGCGGAG 1	618
8 8	460	LysProLysValLysGluIleIleAspGluArgThrArgGluArgLeuValTyrGluVal 4	179
Q C	1619	AAGCCCAAGGTCAAGGAGTTATTGATGAGGGCACAAGAGAGGGGCTGGTGTACGAGGTG 1	678
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ò	520	ysAlaTyrGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrlleCysCysGlyGly 5	339
qq	1799		858
ò	540	ArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGluCysVal 5	659
q	1859	CONCAGGIGCTCATGTGCGGAAACAACTGCTGCAGGTGCTTTTGCGTGGAGTGTGTGT	918
ò	260	AspleuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCys	678
qu	1919	SACCICTTEGIGGGGCCGGGGGCTGCCCAGGCAGCCCATTAAGGAAGACCCCTGGAACTGC	978
ò	580		66
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Best Local Similarity:
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  ProSerAspLeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGlu
                                                                                                             AspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGlnAspSerGly
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1 (bases 1 to 4258)
Ni,J., Pradhan,S. and Roberts,R.J.
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,J., Pradhan,S. and Roberts,R.
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WCTEMERVFGFPVHYTDVSNMSRLARORLLGRSWSVPVIRHLFAPLKEYFACV"
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/product="DNA cytosine
/protein_id="AAL57039.1
/db_xref="GI:18033253"
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/db_xref="taxon:9606"
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셤	1607	AAGCCCAAGGTCAAGGAGATTATTGATGAGCGCACAAGAGAGCGGCTGGTGTACGAGGTG
ò	480	ArgGlnLysCyaArgAsn1leGluAspIleCys1leSerCysGlySerLeuAsnValThr
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ç q	500	500 LeugluhisProLeuPheIleGlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGlu 519
ò	520	CysalatyrdintyraspaspaspAspGlytyrdinsertyrCysfhrileCysGlyGly
8 8	1787	TGTGCGTACCAGTACGACGACGACGACGACTACCAGTCTACTGCACCATCTGGGGGGGG
do do	1847	
ò	560	AspleuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCys
qq	1907	gacciciiggigggcccgggggcigcccaggcagccaiiaaggaggccciggaacigc
දු පු	580	TyrMet.CysG1yHisLysG1yThrTyrG1yLeuLeuArgarghrgG1uAspTrpProSer
ò	009	ArgleuGlnMetPhePheAlaAsnAsnHisAspGlnGluPheAspProbroLysValTyr
Db	2027	cescrecasarstrescraataaccaceaccaeaartreaccrecaaasstrac
ò	620	Proproval ProblacluLysArgLysProlleArgValLeuSerLeuPheAsgGlylle
qq	2087	CCACCTGTCCCAGCTGAGAAGAAGAAGCCCATCCGGGTGCTCTCTCT
<u>ک</u> ۾	640	AlaThxClyLouLeuValLeuLygAbgLeuGlyIleGlnValAppArgTyrIleAlaSer
ò	99	GluValCysGluAspSerIleThrValGlyMetValArgHisGlnGlyLysIleMetTyr
qq	2207	GAGGTGTGTGTGAGGACTCCCATCACGTGGGCATGGTGCGCACCAGGGGAAGATCATGTAC
ò	089	ValGlyAspValArgSerValThrGlnLy8HisIleGlnGluTrpGlyProPheAspLeu
q	2267	GTCGGGGACGTCCGCAGCGTCACAGAAGCATATCCAGGAGTGGGGCCCATTCGATCTG
ò	700	VallleGlyGlySerProCysAsnAspLeuSerIleValAsnBroAlaArgLysGlyLeu
g	2327	GIGATIGGGGGGGGTCCCTGCAATGACCTCTCCATCGTCAACCCTGCTCGCAAGGGCCTC
ò	720	TyrGluGlyThrGlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAlaArgPro
gg	2387	TACGAGGCACTGGCCGGCTCTTCTTTGAGTTCTACGCCTCCTGCATGATGCGGCCCC
કે ફ	740	LysGluGlyAspAspArgProPhePheTrpLeuPheGluAanValValAlaMetGlyVal
ò	760	SerasplysargasplleSerargPheLeuGluSerasnProValMetIleAspAlaLys
g	2507	
ò	780	GluvalSerAlaAlaHisArgAlaArgTyrPheTrpGlyAenLeuProGlyMetAenArg
qq	2567	GAAGTGTCAGCTGCACACAGGGCCCGCTACTTCTGGGGTAACCTTCCCGGTATGAACAGG
ò	800	ProLeuAlaSerThrValAsnAspLysLeuGluLeuGlnGluCysLeuGluHisGlyArg
q	2627	ccgriggcarccacrcrcaarcaraacrccaccaccaccaccaccac
ò	820	IlealalysPheSerLysValArgThrIleThrThrArgSerAsnSerIleLysGlnGly
qq	2687	ATAGCCAAGTTCAGCAAAGTGAGGACCATTACTACGAGGTCAAACTCCATAAAGCAGGGC

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                                            Barbarta, J., Benton, J., Binage, H. C., AFE, J. K., Ayele, M., Barhs, T.,
Barbarta, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
Buck, J., Bowie, S., Brevan, B., E., Byrd, N. C.,
Burch, P., Burkett, C., Burrell, K.L., Byrd, N. C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Datborne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Chtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Lozado, R.J., Lu, K., Lucier, R., Martindale, A., Martinez, B.,
Mabeshwari, M., Mapua, P., Mattin, R., Martindale, A., Martinez, B.,
Mabeshwari, M., Mapua, P., Mattin, R., Martindale, A., Martinez, B.,
Mabeshwari, M., Newtson, S., Oghm, M., Okwonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Petery, J., Petez, L.,
Peters, L., Pickens, R., Primus, B., Pu, L.L., Oulles, M., Ren, Y.,
Scherer, S., Soctt, G., Shen, H., Shooshtari, N., Sisson, I.,
Surton, A., Stanley, H., Stone, H.,
Sunton, A., Wange, C., Washington, C., Watlington, S.,
Walle, S., Walle, K., Monda, S., Wallen, S.,
Walle, S., Walle, K., Marten, R.
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M.,
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                                      Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Weinstock,G. and Gibbs,R.
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16, *** SEQUENCING IN PROGRESS
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Banks,T.,
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Direct Submission
Submitted (23-JUL
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Baylor Plaza, Houston,
3 (bases 1 to 123936)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-JUI-2002) Human Genome Sequencing Center, Depar
of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
On Jul 18, 2002 this sequence version replaced gi:20531783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.) NOTE: This is a "working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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be preserved.
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Center clone name: CH230-282D16
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HisGlnAlaThrTyrAsnLysGlnProMetTyrarg 362 MetThrGlyArgSerArgAlaAlaGluGlyThrArg 322 LysPheSerValValCysValGluLysLeuMetPro 342 ValAlaSerSerArgAlaGlyLysLeuPheProAla 382 ||||||||||||| GTGGCCAGCAGTGTTCAGGGAAGCTGTTCCCAGCG 85308 heGlnProSerGlyProLysGlyLeuGluProProG 422 ArgThrArgGluArgLeuValTyrGluValArgGln 481 3lnSerTyrCysThrlleCysCysGlyGlydrygGlu 541 AlaAlaIleLysGluAspProTrpAsnCysTyrMet 581 LeuleuhrgargargaluaspTrpProSerArgLeu 601 lleArgValLeuSerLeuPheAspGlyIleAlaThr 641 ATCAAGGCAGCTGATGAGGACCCCGAGTATGAGGAT 85012 AspClnGluPhsAspProProLysValTyrProPro 621 spSerGlyLysAlaValGluValGlnAsnLysGlnM 402 lalyslysProArglysSerThrThrGlubys-Pro 461 CysileSerCysGlySerLeuAsnValThrLeuGlu 501 CysGlnAsnCysLysAsnCysPheLeuGluCysAla 521 SysCysArgCysPheCysValGluCysValAspLeu 561

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Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science University of Tokyo, Laboratory of Genome Structure Analysis, Hum Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-k 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science,
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AK025230.1 GI:10437699
oligo capping; fis (full insert sequence).
oligo capping; con cDNA to mRNA, clone_lib:COL clone:COL06724.
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Sugano, S., Suzuki, Y.,
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Okamoto,S., Okitani,R., Ota,T., Suzul
Shibahara,T., Tanaka,T., Nakamura,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                       /tissue_type="colon"
/clone_lib="COL"
                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                       vector pME18SFL3"
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ArgPheLeuGluSerAsnProValMetIleAspAlaLysGluValSerAlaAlaHisArg
                                                                          PhePheTrpLeuPheGluAsnValAlaMetGlyValSerAspLysArgAspIleSer
                                                                                                                                           PhePheGluPheTyrArgLeuLeuHisAspAlaArgProLysGluGlyAspAspArgPro
                                                                                                                                                                                           AATGACCTCTCCATCGTCAACCCTGCTCGCAAGGGCCTCTACGAGGGCACTGGCCGGCTC
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GlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAsp
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AsnAsnAsnCysCysArgCysPheCysValGluCysValAspLeuLeuValGlyProGly
                                                                              GACGGCTACCAGTCCTACTGCACCATCTGCTGTGGGGGGCCGTGAGGTGCTCATGTGCGGA
                                                                                                                 AspGlyTyrGlnSerTyrCysThrIleCysCysGlyGlyArgGluValLeuMetCysGly
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Submitted (27-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 168651)
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902 CGATTTCTCGAGTCCACCCTGTGATGATTGATGCCAAAGAAGTGTCAGCTGCACACAGG 961
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Homo sapiens BAC clone RP11-179G23 from 2, complete sequence.
AC009474
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Center: Washington University Genome Sequencing Center Center Code: WUGSC WESS WUGSC Web site: http://genome.wustl.edu/gsc
                                      787 AlaArgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProLeuAlaSerThrValAsn
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Mulvane, E., Stoneking, T., LaPlant, Y. and McDill, B.
The sequence of Homo sapiens BAC clone RPI1-179G23
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Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.H.
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SOURCE INFORMATION:
The RPG1-11 human BAC library was made from the blood of one male donor, as described by Osocgawa. K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: papac.med.buffalo.edu)
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The clone sequenced to the left is RP11-547F18; the clone sequenced to the left is RP11-547F18; the clone sequenced to the left is RP11-444B4.

Location/Qualifiers
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                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for denetics, Washington University, St. I.
MOPHERSON. Department of Genetics about the map position of this sequence, see http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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/db_xref="taxon:9606"
/chromosome="2"
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3149. 3465
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7819. .7868
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16209. .16345
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32568, 32777
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9304. .9469
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37615. .37715
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26569.
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26074. .26366
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37266. .37340
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14930. .35230
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30824. .31150
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19540. .19659
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[7575...18261
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16513. .16676
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444 TyrAlaProProProAlaLysLysProArgLysSerThrThrGluLys----
                                                                                                     GluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGlu 423
                                                                                                                                                             HisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnLysGlnMetIle
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                            GAGAAGAATCCCAGCAAAGAAGTTTATGCACACGTGAGGGGTGACCCTGAGGCAACTGCT
                                                                                      AGATGGACCTTTGGGGGGGTTCCAGCCTTCTGCCCCCAAGAGACTGGAGCCACAAGAAGAG
                                                                                                                                                                                                    GCCATCTACGAAGTCCTGCCGGTGGCCAGCAGTGT-ACAGGGGAGCTGTTCTCAGGGAGC 75372
                                                                                                                                                                                                                      AlaīleTyrGluValieuGlnValAlaSerSerArgAlaGlyLysLeuPheProAlaCys 383
                                                                                                                                                                                                                                                              TTTTGCAGTGTTCCACCAGACCAC-CTATAATACAACAAGCAGCCCATGTACCACAAA 75313
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                                                      GluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGluAlaAlaAla 443
                                                                                                                                            PheCysSerAlaPheHisGlnAlaThr-----TyrAsnLysGlnProMetTyrArgLys 363
                                                                                                                                                                                                                                                                                                                                         TrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeuSerSer 345
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58109. .58420
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49340. .49621
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48914. .49033
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Submitted (28-MAY-1998) CVRC, Mass. Gen. Hospital, 149 13th Street, Submitted (28-MAY-1998) CVRC, Mass. Gen. Hospital, 149 13th Street, CMARDOWN, MA 02129, USA (Dases 1 to 4135) (Dases 1 to 4135) CVRC, Mass. Gen. Hospital, 149 13th Street, CMARDOWN, CADIAWAT., Sasaki, H. and Li,E. Direct Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street, Sabmitted to 40-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street, Sequence update by submitter on Nov 18, 1999 this sequence version replaced gi:3327981.
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Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmc3b) mRNA,
alternatively spliced, complete cds.
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Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 4135)

Okano, M., Xie, S. and 1i, E.

Cloning and characterization of a family of novel mammalian DNA

(cytosine-5) methyltransferases

Nat. Genet. 19 (3), 219-220 (1998)
                                                 77078 CATTGAAATTGAAAGGGTATTTGGACTCCCTGTCCATTATACTGACATCTCCCAACATAAG 77137
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                                                                                                                                                                                                                                                                                                                               76627 CTC-----------TGCAATGACCTCTCCATTGTCAACCCTGCCCACGA 76664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               857 sThrCluMetGluArgValPheGlyPheProValHisTyrThrAspValSerAsnMetSe 877
                             717 sGlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAl 737
                                                                                                   737 aArgProLysGluGlyAspAspArgProPhePheTrpLeuPheGluAsnValValAlaMe 757
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Db 77198 CTTCCTCCATCAAAGAGGTATTTTGCTTGTTGT 77231
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GGANACAATGAAGGGAĠÁĊAGCAGACATCTGAATGAAGAAGAGGGTGCCAGCGGGTATGA
                                                                                                   nAspSerGlyProSerAsp
                                                                                                                                         CGCGGGATCTCCCCCCCCCATCCATAGTGCCTTGGGACCAAATCCAGGGCCTTCTTTCA
                                                                                                                                                                            lGluSerSerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGl
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SRRRRASSSASTPWSSPASVDFMEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESRD
GDSTEYQDDKEFGIGDLYWGKIKGFSWMPAMVYWSWKATSKRQAMFGMRWYQWFGGGKF
SEISANLVALGLFSOHFULATFUKLVSYRKAMYHTLEKARVRAKTFSKSPGESLED
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KDGSDEESREEMASEVTNNKGNLEDRCLSCGKKUPVSFHLFFEGGLCQSCRDRFLEL
FYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVECLEVLVGAGTAEDAKLQEPWS
CYMCLPQRCHGYLRRKUMNMKLQDFFTTDDDLEEFEPPKLYPAIPAAKKRPIRVLSL
FPMGIATGYLVLKELGIKVEKYIASEVCAESIAVGTVKHBGQIKYVNDVKKITKKNIEE
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ENVVANKVNDKKDISRFLACNPVMIDALKVSAAHRARYEWGNLPGWASKNDKL
ELQDCLEFSRTAKLKKVQTITTKSNSIRQGKNQLFPVVMNGKDDVLMCTELERIFGFP
ANTUVSNMGRGARQKLLGRSWSVVIHHLFAFLKDYFACE"
43 a 1046 C 1106 C 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Dnmt3b"
/note="similar to EST sequences deposited in GenBank
Accession Numbers AA116694, AA119979, AA177277, AA210568,
AA407106, and AA575617"
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  GGAGTGGGCCCACGGTGGCTTCAAGCCTACTGGGATCGAGGGCCTCAAACCCCAACAAGAA
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                                                                                  462 BValLysGluIlelleAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLy
                                                                                                                          482 sCysArgAsnIleGluAspIleCysIleSerCysGlySerLeuAsnValThrLeuGluHi
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and Shen, Y.
                                                  2404 GTCTGCTGCTCACAGGGCCCGGTACTTCTGGGGTAACCTACCCGGAATGAACAGGCCCGT 2463
                                                                                                                                                                                                                 2464 GATGGCTTCAAAGAATGATAAGCTCGGAGCTGCAGACTTGCAGTTCAGTAGGACAGC 2523
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LTRETKDTRTRSESPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQEYPVEFPATR
SRRRASSSASTEWSSPASVDFWEEVTEKSVSTSVDLSQDGDGGMTTQVDAESIY
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SEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
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CYMCLPQRCHGVLRRRKDWMRRLQDFFTTDPLLEFEFPKLYLAGTAEDAKLQEFMS
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FDGIATGYLVLKELGIKVEKYIASBVCAESIAVGTVKHEQGIKYVNDVRKITKKNIES
WGFFDLVIGGSPCNDLSHVNPAARKGLYEGTGRLFFEYHLLNYTRPKEGDNRFFFMMF
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AHYTDVSNMGRGAAQKLLGRSWSVPVIRHLFAPLKOYFACE"

BASE COUNT ORIGIN Percent Similarity:
Best Local Similarity:
Query Match: 밁 á Ś 밁 Ś В Ś 밁 δ 밁 á 밁 ঠ 밁 Ś 밁 á 밁 5 밁 밁 밁 Ś US-09-720-086-5 (1-908) x AF151970 (1-4278) ment Scores: 34S 594 534 525 101 405 285 165 121 465 144 141 765 TGTCCGAACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCAAAGAGCCTCCCCCAG 84 77 57 38 19 4 AAAGCTCACCCGTGAGACCAAGGACACCAGGACGCGCTCT oSerAlaThrAlaArgLysValGlyArgProGlyArgLysArgLysHisPro---ProVa 57 AspArgLysGluGlyGluGluGluGluAsnArgGly-LysGluGluArgGlnGluPr 38 SerGlyProGlyAspThrSerSerSer----gGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArgGlnArgProMetProAr oProGluAlaSerArgAlaValGluAsnGlyCysCysValThrLysGluGlyArgGlyAl 141 nAspSerGlyProSerAsp------CGCGGGATCTCCCCCCCCATCCATAGTGCCTTGGGACCAAATCCAGGGCCTTCTTTCA 404 AGCGGCCCAAGTAAACGTÁGCGCAGCGATCGGCGCCGGAGATTCGCGAAACCCGÁCACTCC 224 AĞĞAĞATĞĞAĞACAĞAĞATGATĞAAĞTAĞATĞATĞĞĞAATĞĞCTCTGATATTCTAATĞCC AAGCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACATGAC aSerAla-----AGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACCAGAGACCAGAGGCCGCAGGTC ySerProAlaAlaGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyThrGluThrPr 121 GGAGTGCATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCC 524 -----LeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGluGl 101 GGAAACAATGAAGGGAGACAGCAGACATCTGAATGAAGAGAGGGTGCCAGCGGGTATGA 464 lGluSerSerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGl CGACAGGCCCGCTGAGGCTTGTGCCAGACCTTGGAAACCTCAGGTATATACCTTTCCAGA 344 -----LysGluGlnLysGlnThrAsnIleGluSerMetLysMetGluGlySerAr 163 -GlyGluGly----1055 ø ELQDCLEFSRTAKLKKVQTITTKSNSIRQGKNQLFPVVMNGKDDVLMCTELERIFGFP AHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE" 1.6e-90 2211.00 61.22% 46.95% 45.04% ი Conservative: Mismatches: Indels: Length: Matches: Gaps: 956 t ----SerLeuGluArgGluAsp 18 -----CC 4278 454 138 266 109 -GAAAGCCCGGC 77 764 713 146 653 143 593 533 83

542 1826	522 rGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrIleCysCysGlyGlyArgGluVa	B 6
522 1766	502 8ProLeuPheIleGlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTy	β δ
502 1706	482 SCYSATGASNIleGluASDIleCYSIleSerCYSGlYSerLeuASnValThrLeuGluHi ::: :::	B 8
482 1646	462 sVallysGluIleIleAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLy	B 8
462 1595	442 aAlaTyrAlaProProProProAlaLysLysProArgLysSerThrThrGluLysProLy	B 8
442 1535	rpValGluProGluAlaAl ;;;;; GACTCTGC	₽ &
423 1490	403 eGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGl	용 성
403 1430	383 sHisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnLysGlnMetIl	B 8
383 1383	eProAlaCy 	B 8
363 1331	/rArgLy \TAGGAA	B 8
343 1271	323 pValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLe	8 8
323 1211	303 oGlyArgIleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTr	유 성
303 1151	283 yArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPr :::	B 성
283 1091	263 yAspAlaGlyAspLysAsnAlaThrLysAlaAlaAspAspGluProGluTyrGluAspGl :	용 성
263 1031	243 GlnGlnProThrAspProAlaSerProThrValAlaThrThrProGluProValGlyGl :	B 성
243 983	223 IGluGluAsnGlnAlaSerGlyGluSerGlnLysValGluGluAlaSerProProAlaVa:	B &
223 929	aVa GCC	용성
203 869	183 gLeuThrPheGlnAlaGlyAspProTyrTyrIleSerLy8ArgLy8ArgAspGluTrpLe	β δ

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2007 AGACTTCTTCACTACTGATCCTGACCTGGAGAATTTGAGCCACCCAAGTTGTACCCAGC
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                                                                                                       sGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrpProSerArgLeuGl
                                                                                                                       nMet PhePheAlaAsnAsnHisAsp---GlnGluPheAspProProLysValTyrProPr
                                                                                                                                                                                                              621 oValProAlaGluLysArgLysProlleArgValLeuSerLeuPheAspGlylleAlaTh
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                                                                                                                                                                                                                                                                                                                      661 lCysGluAspSerIleThrValGlyMetValArgHisGlnGlyLysIleMetTyrValGl
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                                                    562 uValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCysTyrMetCy
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A I CTERTYCT FETRICARSSELLSKEEVES LILLYTODMTGOODDDEVDOONGSDILLMPR
LITRETYCT FETRICARSSELLSKEEVES LILLYTODMTGOODDDEVDOONGSDILLMPR
SRRRAASSASTPWSSERLSKEEVES WAS LILLYTODMTGOODDDEVDOONGSDILLMPR
SRRRAASSASTPWSSERAYUPKEEVTPKSYSTPSYDLSQOODDGOODTTOVDALSEN
GDSTEYODDKEFCJIGDLYWGKIKGFSWRAMMANUSKKATSKROAMPGARFWOMFTGOOKE
SEI SADKLYALGLESOHPHLATPINKLYSYRKAMTHTLERARVRAKTFSSESPESELED
OLKPMIEWAAGGFKTOTSGELKONKKOPVNKSKYRKASDSRNLEDRRISCKSCKKNEYVS
BHPLEFGGLCOSCREDER LELEYMYDBOOYONSKYRKASDSRNLEDRRISCKKRYTVN
BAASESP PPRKLATNSYGKOKDREDEDESBERMAGASTVINKKGILEDRCLICCSKKNEYVS
FHPLEFGGLCOSCREDREFLELEYMYDBOOYOSYCTVCCGRRELLLCSNYTSCCRCFCVEC
LEVLYGAGTAEDAKLQEPWSCYMCLPQRCHGVLRRRKDNNMRLQDFFTTDPDLEEFEP
PKLYPAL PAAKRRP FRULELEDGIATGVINKUSKOTSTNEYN TDATUSKYSTAY
GOOIKYVNDVRATTKKNIEGWGFFDLYTGGSPCNDLSNVNHARRGLYGETGTGRLFFEFF
FWGLNYTPRECEDNRF FFWMFENVVANKVNDKKDIS SEFLAKOPYNTDATKVSAAHRARY
FWGNLPGWNRF PVANKTENDCHOLLEFSTTAKLKKOOTITTYSSSSTANGTYKK
WOGKDDVLWCTELERIFGFPAHYTDVSNWGRGARQKLLGRSWSVPVIRHLFAPLKDYF
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Mes mesolus DNA cytcsine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.
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region; C-ternainal region is similar to corresponding
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/protain id="AACQ178.2"
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/translation="MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
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Xie,S., Okano,M. and Li,E.
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3 (bases I to 4195)
Okano,M., Chijima,T., Sasaki,H. and Li,E.
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                                                                                                                                                                                                                                                                                                                                                            Mus musculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.

(bases 1 to 4195)

(kano, M., Xie, S. and Li, E.

Cloning and characterization of a family of novel mammalian DNA

(cytosine-5) methyltransferases

Nat. Genet. 19 (3), 219-220 (1998)
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Accession Numbers All16694, Aal19979, Aal77277, AA210568,
And7106, and AA575617"
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Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327979.
Location/Qualifiers
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/db_xref="taxon:10090"
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/gene="Dnmt3b"
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2907 GAAGGACTACTTTGCCTGT 2925
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GGAGACGTCGAGCATCGTCTTCAGCAAGCAC erGlnLysValGluGluAlaSerProProAl : :	203 uAlaArgTrpLysArgGluAlaGluLysLysAlaLysValIleAlaValMetAsnAla	Oy 183 gLeuThrPheGlnAlaGlyAspProTyrTleSerLysArgLysArgAspGluTrp	Qy 163 gGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArgGlnArgProMetProA	Oy 147LysGluGlnLysGlnThrAsnIleGluSerMetLysMetGluGlySerAr	OY 144 -GLYGIUGLY	141 ASEXALA : ::: 451 AAGCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACATG	y 121 o	Qy 101 ySerProAlaAlaGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyThrGluThr	4LeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGl 	Qy 77 nAspSerGlyProSerAsp	Qy 57 lGluSerSerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaG	QY 38 oSerAlaThrAlaArgLysValGlyArgProGlyArgLysArgLysHisProProV	uGluAspArgGly-LysGluGluArgGlng 	Qy 4 SerGlyProGlyAspThrSerSerSerSerLeuGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGraccGAGGCGAGGCGAGGGCGAGAGTGGGGGGGGGGGGGGGG	US-09-720-086-5 (1-908) x AF068626 (1-4195)	Alignment Scores: 2.62e-90 Length: 4195 Score: 2206.00 Matches: 455 Percent Similarity: 59.78\$ Conservative: 135 Best Local Similarity: 46.10\$ Mismatches: 268 Query Match: 44.94\$ Indels: 129 DB: 16	BASE COUNT 1061 a 1059 c 1125 g 950 t ORIGIN
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582 sGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrpProSerArgLeuGl 602	Ş
GGGCGCAGGCACAGCTGAGGATGCCAAGCTGCAGGAACCCCTGGAC	ఠ
ValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCysTyrMetC	Q V
44 GCTGCTGTGCAGTAACACAAGCTGCTGCAGATGCTTCTGTGTGGAGTGTCTGGAGGTGCT 18	문 .
LeuMetCvsGlvAsnAsnAsnCvsCvsArqCvsPheCvsValGluCvsValAst	Ş
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22 rd]nTvr&sp&sp&sp@sp@lvTvrQlp&srTvrCvsThrl]eCvsCvsGlvGlv&rdGlnVa 54	Ş
	당 :
02 sProLeuPhelleGlvGlvMetCvsGlnAsnCvsLvsAsnCvsPheLeuGluCvsAlaTv 52	Ş
482 SCYBATGABNILECYTILECYTILECYTILECTYSCLYSETLEUASIVALINITLEUGLUHI 502	B 5
13 AGGGGAGGATGAGGAGAGCCGAGAACGGATGGCTTCTGAAGTCACCAACAA 15) D
62 sValLysGluIleIleAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLy 48 : ::: :::	Ş
1453 TGCTTCTGAGTCCCCCACCCAAGCGCCTCAAGACAAATAGCTATGGCGGGAAGGACCG 1512	망
442 aAlaTyrAlaProProProProAlaLysPysProArgLysSerThrThrGluLysProLy 462	Q
1408 GAGACGCGAGAACAAAAGTCGAAGACGCACCAAT	ఠ
422 uGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGluAlaAl 442	Ş
1348 GCAACCAGTGGTTAATAAGTCGAAGGTGCGTCGTTCAGACAGTAGGAACTTAGAACCCAG 1407	助
421ProGl 422	Ş
1288 GGAGTGGGCCCACGGTGGCTTCAAGCCTACTGGGATCGAGGGCCTCAAACCCCAACAAGAA 1347	дb
403 eGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluPro 420	ş
1241TCCAGCAGTCCTGGAGAGTCACTGGAGGCCAGCTGAAGCCCATGCT 1287	ర్జ
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1189 GGCCATGTACCACACTCTGGAGAAAGCCAGGGTTCGAGGTGGCAAGACCTTC 1240	Дb
AlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLe	Ş
1129 GGGGCTGTTCAGCCAGCACTTTAATCTGGCTACCTTCAATAAGCTGGTTTCTTATAGGAA 1188	Дb
sGlnAlaThrTyrAsnLysGlnProMetTyrAi	Ş
1069 GGTACAGTGGTTTGGTGATGGCAAGTTTTCTGAGATCTCTGCTGACAAACTGGTGGCTCT 1128	da
valwetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeumetProL	δ
AAAGCCACCTCCAAGCGACAGGCCATGCCCGGAATG	Дb
lSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrA	Ş
AGTTTGGAATAGGTGACCTCGTGTGGGGAAAGATCAAGGGCTTCTCCTGG	90
pheGlYIleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpT	Qy
CCACACAGGTGGATGCAGAGAGAGAGAGAGGAGAGAGAGA	В
63 yAspAlaGlyAspLysAsnAlaThrLysAlaAlaAspAspGluProGluTyrGluAspGl 2	γQ
841 CAGTACCCCATCAGTTGACTTGAGCCAGGATGGAGATCAGGAGGGTAT 888	망
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Submitted (17-MX-1999) Department of Biochemistry and Molecular Biology, Institution of Basic Medical Sciences, Chinese Academy of Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4338)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and Shen, Y.
                                                                                                                                                                                                                                                                                                                                                            /product="DNA cytosine-specific methyltransferase isoform
                                                                                          Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue
Unpublished
2 (bases 1 to 4338)
2 (hases 1 to 4338)
3 Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. an Shen, Y.
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                                                                                                                                                                                                                                                                                                                                  function="methylates cytosine in DNA"
note="alternatively spliced"
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Matches:
Conservative:
Mismatches:
Indels:
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/dev_stage="8-9 day old embryo"
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/gene="Dnmt3b"
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/organism="Mus musculus"
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/gene="Dnmt3b"
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Mus musculus
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                                                                              621 oValProAlaGluLysArgLysProIleArgValLeuSerLeuPheAspGlyIleAlaTh
                                                                                                                        rGlyLeuLeuValLeuLysAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluVa
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323 pValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLe 343	D 8
303 oGlyArgIleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTr 323	B 8
283 yArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPr 303 ::: :::	다. 양 양
263 YASBALAGIYASBIYSASRALATHYEALAALAASBASBGUUPROGUUTYTGIUASBGI 283 	B &
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LysValGluGluAlaSerProProAlaVa 2 ::: :::	ş 8
203 uAlaArgTrpLysArgGluAlaGluLysLysAlaLysValIleAlaValMetAsnAlaVa 223	
183 gLeuThrPheGlnAlaGlyAspProTyrTyrIleSerLysArgLysArgAspGluTrpLe 203	B &
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14 ANAGCTCACCCGTĠĀĠACCĀĀĠGACĀĆĊĀGGĀCGCGCTĊTĠĀĀĀGCCCGGC 7	문
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TIGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACATGA	gg
141 aSerAla 143	Ş
121 oProGluAlaSerArgAlaValGluAsnGlyCysCysValThrLysGluGlyArgGlyAl 141	gb Qy
101 ySerProAlaAlaGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyThrGluThrPr 121	B -0
465 GGAGTGCATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCC 524	Вb
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77 nAspSerGlyProSerAsp	4g VQ
S CGCGGGATCTCCCCCCCCATCCATAGTGCCTTGGGACCAAATCCAGGGCCTTCTTTCA 4	₽ .
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701	681 yAspValArqSerValThrGlnLysHisIleGlnGluTrpGlyProPheAspLeuValIl	ş
2306	T CTGTGCAGAGTCCATCGCTGTGGGAACTGTTAAGCATGAAGGCCAGATCAAATATGTCAA	당 성
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661 2246	641 rGlyLeuLeuValLeuLysAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluVa 	음 성
641 2186	621 oValProAlaGluLysArgLysProIleArgValLeuSerLeuPheAspGlyIleAlaTh ::: :::	β Q
621 2126	602 nMetPhePheAlaAsnAsnHisAspGlnGluPheAspProProLysValTyrProPr	₽ Q
602 2066	582 sGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrpProSerArgLeuGl 	B &
582 2006	562 uValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCysTyrMetCy	8 8
562 1946	542 lLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGluCysValAspLeuLe	B &
542 1886	522 rGlnTyrAspAspAspAspGlyTyrGlnSerTyrCysThrIleCysCysGlyGlyArgGluVa	유 성
522 1826	502 sProLeuPheIleGlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTy	B 8
502 1766	482 sCybArgAsnIleGluAspIleCysIleSerCysGlySerLeuAsnValThrLeuGluHi 	B 8
482 1706	462 sVallysGluIleIleAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLy : :: :: 1656 AGGGGAGGATGAGGAGAGCCGAGAACGGATGGCTTCTGAAGTCACCAACAA	B 8
462 1655	442 aAlaTyrAlaProProProProAlaLysLysProArgLysSerThrThrGluLysProLy	B &
442 1595	422 uGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGluAlaAl	용 성
422 1550	421	B 8
420 1490	403 eGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLySGlyLeuGluPro	D 64
403 1430	383 sHisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnLysGlnMetIl	유양
383 1383	363 sAlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProAlaCy ::: ::: 1332 GGCCATGTACCACTCTGGAGAAAGCCAGGGTTCGAGCTGGCAAGACCTTC	망양
363 1331	343 uSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLy	B 8

1xon:10090" 18-9 day old embryo"

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FEATURES Location/Qualifiers 1. 4163 FEATURE Autoranism = Mus muscul FEATURE = Mus muscul FEATURE = Mus muscul FEATURE = Muscul = Mus	/ protein_id="AAF74520 / db_xref="d::847131" / translation="WKGDSRH / translation="WKGDSRH AICTEPVCTPETRGRESSRL AICTEPVCTPETRGRESSRL AICTEPVCTPETRGRESSRL AICTEPVCTPETRGRESSRL AICTEPVCTPETRGRESSRL ABTRANSSSATPWSSPAYNING CDSTEWNINGETRGREGORICHION CDSTEWNINGETRGREGORICHION CDSTEWNINGETRGREGORICHION CDSTEWNINGETRGREGORICHION CDSTEWNINGETRGREGORICHION CDSTEWNINGETRGREGORICHION ELODCLEFSRTAKLKKOTTT AHYTDVSNMGRGARROKLIGRS ARTDVSNMGRGARROKLIGRS AHYTDVSNMGRGARROKLIGRS AHYTDVSNMGRGARROKLIGRS AHYTDVSNMGRGARROKLIGRS ORIGIN	Alignment Scores: Pred. No.:	Db 130 CGCACGGGCCTCCAGATCCGGGGGGGGGGGGGGGGGGGG
	761 pLysArghepileSerArgheLeuGluSerAsnProValMetileAspAlaLysGluVa 7	Qy 861 UARGVAlPheGlyPheProValHisTyrThrAspValSerArgLeuAlaAr 881 Db 2847 AAGGATCTTCGGCTTCCCTGCTCACCACGACGTGTCCACAATGGGCGGGGCGCGGGCCCG 2906 Qy 881 GGInArgLeuLeuGlyArgSerTrpSerValProValIleArgHisLeuPheAlaProLe 901 Db 2907 TCAGAAGCTGCTGGAGGTGTACCGGTCATCAGACACTTTTGCCCCTT 2966 Qy 901 ULyGGUTYrPheAlaCys 907 Db 2967 GAAGGACTACTTGCCTGT 2985	RESULT 12 AF151974 AF151974 AF151974 AF151974 AF151974 MARGERIAN DEFINITION MARGINAL COMPLETE Cds. ACCESSION VERSION VERSION AF151974.1 GI:8347130 AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 MARGINER DEFINITION AF151974.1 GI:8347130 AF151974.1 GI:83410 AF151974.1 GI:83410 AF151974.1 GI:83410 AF151974.1 GI:83410 AF151974.1 GI:83410 AF151974.1 GI:83410 A

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                                                                                                                                                                                                         NA cytosine-specific methyltransferase isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGACACGAAGGATGCTCCCTCACCC----- 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------CCAGTCTTGGAGGCAATCTGC 437
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GCGCCGGGGTTAAGCGGCCCAAGTAAACGTAGCGCAG 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ......LeuLeuProAsn 87
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methylates cytosine in DNA"
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t=1
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sp 488	GluArgThrArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnileGluAs	469	Ş
AT 1490	CCAAGCGCCTCAAGACAAATAGCTATGGCGC	1440	밁
3p 468	sLysProArgLysSerThrThrGluLysProLysValLysGluIleIleA	449	Ş
4	::: 	1395	맖
CO 448	luValTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProP	429	Ş
T 13	AGCCTACTGGGATCGAGGGCCTCAAACCCCAACAAGAAGCAACCCGAGAACA	1335	Db 5
408	heGlnProSerGlvProLvsGlvLeuGluProProGluGluGluLvsAsnPro	4	Ş
()—- ω	GTCCTGGAGAGTCACTGGAGGGGACCAGCTGAAGCCCATGCTGGAGTGGGCCCA	7	뮹
4	yLysAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeu	390	ş
C 12	::	1236	망
er 389	nValAlaSerSerArgAlaGlyLysLeuPheProAlaCys	370	8
eu 369 	PheHisGinAlaThrTyrAsnLysGinProMetTyrArgLysAlaIleTyrGluValLeu	350 1176	용 왕
AC 1175	AAGTTTTCTGAGATCTCTGCTGACAAACTGGTGGCTCTGGGGCTC		D
la 349	GlyLysPheSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAl		ş
YT 1115	ACCTCCAAGCGACAGGCCATGCCCGGAATGCGCTGGGTACAGTGGTTT	1056	뭣
sp 329	luGlyThrArgTrpValMetTrpPheC	310	Ş
3G 1055	GACCTCGTGTGGGGAAAGATCAAGGGCTTCTCCTGGTGGCCTGCCATGGTGGTGTCCTGG	996	ర్జ
CP 309	yPheSerTrpTrpProGlyArgIleValSe	290	Ş
99	GCAGAGAGCATATATGGAGACAGCACAGAGTATCAGGATGATAAAGAGTTTGGAATAGGT	936	В
LY 289	laThrLysAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyI	270	Ş
T 935	 	879	В
sn 269	rProThrValAlaThrThrProGluProValGlYGlYAspAlaGlyAspLys	250	Ş
878	 AAGAAGTGACACCTAAGAGCGTCAGTACCCCA	834	뮍
ro 249	ProProAlaValGlnGlnProTh	230	γQ
3C 833	GCAAGC	774	ď
	MetAsnAlaValGluGluAsnGlnAlaS	210	Ş
C 77	- CAGGAGTACCCTGTGGAGTTTCCGGCTA	.729	D
lu 209	,AspGluTrpLeuAlaArgTrpLysArgG	190	Ş
4G 728	ANTGGGACCTCCAGCTTGGAGAGGCAAAGAGCCTCCCCCAGAATCACCCGAGGTCGGCA	669	В
ly 189	rpGluSerSerLeuArgGlnArgProMetPr	170	Ş
3C 668	GACACCAGGACGCGCTCTGAAAGCCCGGCTGTCCGAACCCGACL	618	В
ly 169	sGlnThrAsnIleGluSerMetLysMetGluGlySerArgGlyArg	150	Ş
CC 617	GAAGTAGATGATGGGAATGGCTCTGATATTCTAATGCCAAAGCTCACCCGTGJ	558	뮍
ln 149		147	Ş
\T 557	AGGACATO	498	망
146	luGly	144	Ş

828 ThrileThrThrArgSerAsnSerIleLysGlnGlyLysAspGlnHisPheProValPhe 847	8
2511 AAGCTCGAGCTGCAGGACTGCCTGGAGTTCAGTAGGACAGCAAAGTTAAAGAAAG	DЬ
sLeuGluLeuGlnGluCysLeuGluHisGlyArgIleAlaLysPheSerLysValAr	γο
788 ArgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProLeuAlaSerThrValAsnAsp 807	94 VQ
768 PheLeuGluSerAsnProValMetIleAspAlaLysGluValSerAlaAlaHisArgAla 787 	B &
748 PheTrpLeuPheGluAsnValValAlaMetGlyValSerAspLysArgAspIleSerArg 767 	dg VQ
728 PheGluPheTyrArgLeuLeuHisAspAlaArgProLysGluGlyAspAspArgProPhe 747	B &
708 AspLeuSerIleValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhe 727 	B &
688 GlnLysHisIleGlnGluTrpGlyProPheAspLeuVallIeGlyGlySerProCysAsn 707 ::: ::: ::: ::	dg VQ
668 ValGlyMetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValThr 687	A A
648 AspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValCysGluAspSerIleThr 667	40 VQ
628 LysProlleArgValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLys 647 :::	P 64
609 HisAspGlnGluPheAspProProLysValTyrProProValProAlaGluLysArg 627	B 8
589 GlyLeuLeuArgArgAluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsn 608	p 6
569 GlnAlaAlaIleLysGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyr 588 :::	dd VQ
549 AsnCysCysArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAla 568	4g VQ
529 TyrGlnSerTyrCysThrIleCysCysGlyGlyArgGluValLeuMetCysGlyAsnAsn 548	рь Оу
509 MetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspAspGly 528	B &
489 IleCysIleSerCysGlySerLeuAsnValThrLeuGluHisProLeuPheIleGlyGly 508	B 8
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Muzny, D. M. Adang, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alabrachar, D. M. Adang, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alabrachar, J., Benker, J., Benker, J., Benker, J., Benker, J., Benker, J., Benker, J., Benker, J., Benker, J., Burch, P., Burch, P., Burker, C., Burch, E., Brown, M., Eryan, N. C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Byrd, N.C., C., Chen, R., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Dargardo, C., Davy-Carroll, L., Dederich, D. A., David, R., Barnarde, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., Edgard, C., E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176697 bp DNA linear HTG 13-JUL-2002 Sattus norvegicus clone CH230-28122, *** SEQUENCING IN PROGRESS AC112586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat.
Ratus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                       2690
                                                                                                                                                                                                                                                                                                        2751 TCCTGGAGTGTACCGGTCATCAGACACCTGTTTGCCCCCTTGAAGGACTACTTTGCCTGT 2810
    2571 ACAATAACCACCAAGTCGAACTCCATCAGACAGGGCAAAAACCAGCTTTTCCCTGTAGTC 2630
                                                                                                                                                                                                                                                      887
                                                                                                                                                                                                                                                                                                                                                                                                                         888 SerTrpSerValProValIleArgHisLeuPheAlaProLeuLysGluTyrPheAlaCys 907
                                                                                   848 MetAsnGluLysGluAspIleLeuTrpCysThrGluMetGluArgValPheGlyPhePro
                                                                                                                                     2631 ATGAATGGCAAGGACGACGTTTTGTGGGGCACTGAGCTCGAAAGGATCTTCGGCTTCCCT
                                                                                                                                                                                                                                                           868 ValHisTyrThrAspValSerAsnMetSerArgLeuAlaArgGlnArgLeuLeuGlyArg
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AC112586/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
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ACCESSION VERSION KEYWORDS REFERENCE AUTHORS REFERENCE AUTHORS TITLE

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tem.cdu/docs/Genbank draft data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                         A (Day, K.C. Direct Submission Submitted (13-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:20303171.

Center: Baylor College of Medicine Center Center code: BCM

Center code: BCM

Center code: BCM
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 17669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: GRAT

Center clone name: CH30-020122

Center clone name: CH30-020122

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 121959 bases at least Q40

Consensus quality: 120371 bases at least Q30

Consensus quality: 130428 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 1415 bp in length

gap of unknown length

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contig of 1163 bp in length

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contig of 1760 bp in length

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contig of 1522 bp in length

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contig of 1352 bp in length

gap of unknown length

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Contact: hgsc-help@bcm.tmc.edu
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th tenge	unknown	o :	1144	34	*	
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length	unknown	ם ב	0468	458	*	
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ni d	of 2682	Ľ,	0113	845		
length	unknown	ם ב	84.5	835	*	
ength	unknown	פינ	455	44.6	* *	
	of 2662	contig	445	179	*	
+ 3	of 1802	2 5	169	989	* *	
ength	unknown	g	989	979	*	
length bp in length	unknown	다. 0	87081:	86982 87082	• •	
מושלים	of 2085	nti	698	489		
bp in length length	or 2397	օբ	489	479	* *	
ength	unknown	- 0	2399	230		
bp in length	of 1802		229	049		
1 1	of 3711	, E	0397	899	* *	
ength	unknown	- 0	9899	859	· *	
bp in length	of 2081	۲. c	658	450	•	
ri g	of 2854	, <u>C</u> .	4405	155	* *	
ength	unknown	0	1551	145	*	
Length hn in length	of 1953	Ι.ο	145	949	* 1	
ğ	of 2534	μ.	9398	989	٠ *	
ength	unknown	0	6864	676	*	
bo in length	of 2379	contiq	676	438	* 1	
ğin	of 2011	n ti	4285	227	* *	
ngth	unknown	٥	2274	217	*	
bp in length	of 1864	μ,	217	031	*	
* 5	Or 2665	2 5	0120	221		
ength	unknown	-0	7545	744	• •	
תנ תנ	of 1711	۲.,	744	573	*	
length	unknown	o۲	573	563	*	
ength	unknown	· O	389	379	+ +	
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bp in length	of 2222	5 5	187	1965	* *	
ength	unknown	0	965	955		
bo in length	of 2096	۲. c	955	745	* :	(
ניי	of 2281	, C.	735	507	• •	
th	unknown	0 1	507	497	•	
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ğin	of 2060	onti	85.5	649	*	
5	unknown	ap o	649	639	*	
ength	unknown	ap o	427	418	* *	
φĭn	of 1814	onti	417	236		
יבץ זו דפזוקר	unknown	ap o	236	226	*	
ength	125	ap o	307	007	* *	
11.0	on.	contig	997	837	*	
length	Mou	ap o	837	827	+	

																		
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710 rI	18 069 18 6908	670 tV ; 3129 AC	650 YI 3189 CA	630 e# } 3249 CC	610 I	590 3369	570 aa 3411 AC	550 BC	530 ns 3531 GI	510 gG 3591 CC	490 81 3651 TA	470 gTh 3711 CGC	451 Lys	431 3822	411 C 3882 C	391 3941	-720-0	Simi cal S atch:
leValAs	:IleGlnG1 ATCCAGGA	tValArgHisG : AGTGCGGCACC	yIleGlnValAsp CATCCAAGTGGAC	ArgValLeuS CACGTGCTATO	GlnGluPh ::: CCAGAAATT	uLeuArgAr GCTGCGGAG	aAlaIleLys AGCCATTAAC	BCYSArgCY CTGCAGGTG) ::: CCTTCTG	lnAsnCy ACAACTO	silesercy TATCTCATG	rargg aagat	AA H	ValTyrThr GTTTACACC	lnProSerGly:	rGly TCGC	86-5 (1-	larity: imilari
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Homo sapiens DNA cytosine methyltransferase 3 beta (DNWT3B) mRNA,
complete cds.
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1 (bases 1 to 4335)

Ni,J., Pradhan,S. and Roberts,R.J.

Cloning, expression and characterization of human DNMT3 genes
Unpublished

Ni,J., Pradhan,S. and Roberts,R.J.

Chases 1 to 4335)

Ni,J., Pradhan,S. and Roberts,R.J.

Birect Submission
Submitted (12-2000) New England Biolabs, 32 Tozer Road,
Beverly, MA 01915, UBA

Location/Qualifiers
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CPAPKRIKTNCYNNGKORGOEDOSREOWASDVANNKSSLEDGGLSGGRKNPVSFHPLE
EGGLGCYCRARFLELFYWYDDOROGYSYTVCCEGRRELLLSCASTSCCREFCVECLEUJU
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1167 9 951 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 GCGATCGGCCGGAGATTCGCGAGCCCAGCGCCTTGCACGGCCCCAGCCGGCCTCCCG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 GGCGGCAACGCTGCCCGGCCGGCAGCGCTGGGGTTAAGTGGCCCAAGTAAACCTAGCTCG 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --------GluGlySerProAlaAlaGlyGlnLys--- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 GAAAGCATGAAGGGACACCAGGCATCTCAATGGAGAGGACGACGCCGGCGGGAGGAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GlyGlyAlaProAlaGluGlyGluGlyThrGluThrProPro--- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 CTGGAGGCTATCCGCACCCCGGAGATCAGAGGCCGAAGATCAAGCTCGCGACTCTCCCAAG 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 GlyLysGluGlnLysGlnThrAsnIle--------GluSerMetLys 158
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199 ArgAspGluTrpLeuAla---ArgTrp------

544 MetCysGlyAsnAsnCysCysArgCysPheCysValGluCysValAspLeuLeuVal 563 	B 8
524 TyraspaspaspglyTyrGlnSerTyrCysThrIleCysCysGlyGlyargGluValLeu 543	g 8
7 504 LeuPheIleGlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTyrGln 523	g 8
484 ArgAsnileGluAspileCysileSerCysGlyS- ::::: 1606 AGCAGCCTGGAAGATGGCTGTTTGTCTTGTGGCA	B 8
464 LysGITLITEITEARPGITLARGITLARGGITLARGGEWAITYFGWALAIGGITLASCYS 4	
1495 TACTGCCCCGCACCCAAGCGCCTCAAGACAAATTGCTATAACAACGGCAAAGACCGAGGG 15	
1435 TCAAGGAAATACGAGAACAAGACTCGAAGACGCACAGCTGACGACTCGACCACTCTGAC 14	!
13/5 ARCACCCARCCAGTGGTTAATAAGTCGAAGGTGCGTCGTCGTGCAGGCAG	
422 GluGluGlu 424	
1315 ATGTTGGAGTGGGCCCACGGGGGCTTCAAGCCCACTGGG	
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82 AlaCysHisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnLysGln 4	Ş
1216 CGAAAAGCCATGTACCATGCTCTGGAGGAAAGCTAGGGTGCGAGCTGGCAAGACCTTCCCC	_
rgiysalaileTyrGluValieuGlnValalaSerSerArgAlaGlyiysieuPhePro :	γQ
342 ProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyr 361	당 상
1096 CGGTGGGTTCAGTGGTTTGGCGAAGTTCTCCGAGGTCTCTGCAGACAAACTGGTG 11	-
322 ArgTrpValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMet 3	Ş
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302 TrpProGlvArgIleValSerTrpTrpMetThrGlvArgSerArgAlaAlaGluGlvThr 321	g S
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AspAlaGlyAspLysAsnAlaThrLysAlaAlaAspAspGluProGluTyr	ş
246 PROTINASEPROALASERPROTINIVALALATINI	유 성
30 TCACAGACGACACAGAGGACACACATGGGACGCCCCAGAGCAGCAGTACCC 88	뮹
26 AsnGlnAlaSerGlyGluSerGlnLysValGluGluAlaSerProProAlaValGlnGln 24 :::	8
770 CAACAGCATCGGCAGGAACGCCATGGCCGTCCCCTCCCAGCTCTTACCTTACCATCGACC 829	дb

	904 TyrPheAlaCys 907 2866 TACTTTGCATGT 2877	g d
euLysGlu 903 ::: TGAAGGAC 2865	884 LeuLeuGlyArgSerTrpSerValProVallleArgHisLeuPheAlaProLet 	8 8
rgGlnArg 883 ::: GCCAGAAG 2805	864 PheClyPheProValHisTyrThrAspValSerAsnMetSerArgLeuAlaA. 	B 8
31uArgVal 863 ::: 9AAAGGATC 2745	844 PheProValPheMetAsnGluLysGluAspIleLeuTrpCysThrGluMetG	g 8
spGlnHis 843 :: aCCAACTT 2685	824 SerLysValArgThrIleThrThrArgSerAsnSerIleLysGlnGlyLysAss	ß &
laLysPhe 823 CCAAGTTA 2625	804 ThrValAsmAspLysLeuGluLeuGlnGluCysLeuGluHisGlyArgIleA	유 성
euAlaSer 803 :: :: TGATAGCA 2565	784 AlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProLu 	유 성
alserAla 783 TTTCTGCT 2505	764 AsplieSerArgPheLeuGluSerAsnProValMetIleAspAlaLysGluVa	g 9
spLysArg 763 ACAAGAGG 2445	744 AspArgProPhePheTrpLeuPheGluAsnValValAlaMetGlyValSerA:	B 8
luGlyAsp 743 GGGTGAT 2385	724 GlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAlaArgProLysGl 	8 8
luGlyThr 723 \GGGTACA 2325	704 SerProCysAsnAspLeuSerIleValAsnProAlaArgLysGlyLeuTyrGl 	당 성
leGlyGly 703 TGGCGGA 2265	684 ArgSerValThrGlnLysHisIleGlnGluTrpGlyProPheAspLeuValII. 	B 8
lyAspVal 683 \CGACGTG 2205	664 AspSerIleThrValGlyMetValArgHisGlnGlyLysIleMetTyrValGl	용왕
1 CysGlu 663 GTGTGAG 2145	644 LeuValLeuLysAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValValValValValValValValValValValValValV	8 성
rGlyLeu 643 AGGCTAC 2085	624 AlaGluLysArgLysProIleArgValLeuSerLeuPheAspGlyIleAlaTh ::: :::	음 성
CATTCCC 2025	604 PhePheAlaAsnAsnHisAspGlnGluPheAspProProLysValTyrProPr 1966 TTCTTCACCAGTGACACGGGGCTTGAATATGAAGCCCCCAAGCTGTACCCTGC	8 8
JeuGlnMet 603	584 HisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrpProSerArgLe	유 성
tCysGly 583	564 GlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCysTyrMet. 	B &

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                     4223 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 5 AFIS1971
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
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2 (Dases 1 to 4223)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
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/note="alternatively spliced"
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54 -----HisProProValGluSerSerAspThrProLysAspProAlaValThrThrLys 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheGlnProSerGlyProLysGlyLeuGluPro--------
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GTGGGAACTGTTAAGCATGAAGGCCAGATCAAATATGTCAATGACGTCCGGAAAATCACC
                                                                                                                                                                LysProIleArgValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLys
                                                                                                                                                                                                                                                                                                       GlyLeuLeuArgArgArgGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCTGTTTGTCCTGTGGAAAGAACAACCCTGTGTCCTTCCACCCCCTCTTTGAGGGTGGG 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProAlaLysLysProArgLysSerThrThrGluLysProLysValLysGluIleIleAsp 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCTGCTGCAGATGCTTCTGTGTGGAGTGTCTGGAGGTGCTGGTGGGCGCAGGCACAGCT
                                                                                                                                        AGGCCCATTAGAGTCCTGTCTCTGTTTGATGGAATTGCAACGGGGTACTTGGTGCTCAAG
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907 2870	888 SerTrpSerValProVallleArgHisLeubheAlaProLeuLysGluTyrPheAlaCys	8 8
887 2810		B. 8
867 2750	848 MetAsnGluLysGluAspIleLeuTrpCysThrGluMetGluArgValPheGlyPhePro	g 99
847 2690	828 ThrileThrThrArgSerAsnSerIleLysGlnGlyLysAspGlnHisPheProValPhe	유 성
827 2630	808 LysLeuGluLeuGlnGluCysLeuGluHisGlyArgIleAlaLysPheSerLysValArg	8 8
807 2570	788 ArgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProLeuAlaSerThrValAsnAsp	β Q
787 2510	768 PheLeuGluSerAsnProValMetIleAspAlaLysGluValSerAlaAlaHisArgAla	B 8
767 2450	748 PheTrpLeuPheGluAsnValValAlaMetGlyValSerAspLysArgAspIleSerArg	B 8
747 2390	728 PheGluPheTyrArgLeuLeuHisAspAlaArgProLysGluGlyAspAspArgProPhe	유 성
727 2330	708 AspLeuSerIleValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhe	ρ ₀ γ
707	688 GlnLysHislleGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAsn ::: ::: :::	g y

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SUMMARIES
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AAI87804	ABL32171	ABS15085	AAI07545	AAI47141	AAI21858	AAK41092	AAK15369	ABA34009	ABA66923	ABA49011	ABN51598	AA185778	ABS02382	AAI02414	AAI33860	AAI12506	AAK27928	AAK02490	ABA23961	\mathbf{r}	ABA43755	4	ABL82861	ABL64228	ABN97389	AAH05250	AAC77455	AAF82964	AAI85785	ABA13731	AAS86166	ABA20255	AAT21884	053	AAS86165
Human polynucleoti	Human immune syste	Human genome-deriv	Probe #7536 used t	used	Probe #11791 for g		brain e	Probe #12475 for g			Mouse spliced tran		genome-deri	#2405 used	#2546 used	#2439	bone m	brain	#2427 f	foetal	breast c		Human ovarian canc	ch cancer r	#3887				polynuc	Human nervous syst	DNA encoding novel	Human nervous syst			DNA encoding novel

ALIGNMENTS

AAZ37095;

AAZ37095 standard; DNA; 4192 BP

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25-JUN-1998;
24-JUL-1998;
                                                                                                                             Mus sp.
                                                                                                                                           carcinoma; sarcoma; leukaemia; DNA methylation; ss.
                                                                                                                                                  De novo DNA cytosine methyltransferase; Dnmt3a; neoplastic disorder;
                                                                                                                                                               DNA encoding
                                                                                                                                                                              27-MAR-2000
                                                       29-DEC-1999.
                                                                     WO9967397-A1.
        (GEHO ) GEN HOSPITAL CORP
                                         25-JUN-1999;
                                                                                                                                                                de novo DNA cytosine methyltransferase Dnmt3a
                                                                                                                                                                              (first entry)
                    98US-0090906.
98US-0093993.
                                         99WO-US14373
                                                                                                       Location/Qualifiers 217..2943
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Result No.

Score

Match

Length

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Description

Query

4181.4 2871.8 1814 757.8 749.8 559 547.6 482.8

99.7 68.5 43.3 18.1 17.9 13.3 13.3 19.9

2938 4195 4145 709

AAZ37095 AAZ37097 ABL90391 AAZ37096 AAZ37098 ABQ57540

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Human colon cancer
Human colon cancer
Human cDNA sequenc

reproductive

AAH33860 AAH14009 AAL00271

The present sequence encodes a murine de novo DNA cytosine methyltransferase designated Dnmt3s. The polypeptides can be administered therapeutically, especially by expressing encoding polymucleotides, to treat diseases associated with DNA cytosine methyltransferase, such as neoplastic disorders e.g. carcinomas, sarcomas and leukemias. They can be used to disgnose, or determine susceptibility to neoplastic disorders, by assaying for polypeptide expression levels in mammalian cells/body fluids. They are useful to soren for compounds inhibiting/activating the polypeptide. The polypeptide can also be used for in vitro de novo requiate DNA. Such in vitro methylation may be used to direct or regulate DNA expression in biological systems, e.g. recombinant DNA methylated in vitro may be introduced into a cell/organism to increase or decrease expression of a desired polypeptide for which the native DNA is under-methylated or nor methylated. The polypeptides can also be used to produce antibodies which are useful to detect and purify the polypeptide or therapeutically e.g. to treat neoplastic disorders. The polynucleotides are useful to produce probes and primers which are New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias Claim 8; Fig 1A; 114pp; English Okano M, Xie WPI; 2000-106298/09. P-PSDB; AAYS4055. Li E,

Sequence 4192 BP; 1095 A; 1070 C; 1182 G; 844 T; 1 other;

ö 240 240 300 360 420 420 480 600 180 180 300 360 480 61 GCCCAGCGCTGAGGCTGCACTTTTCCGAGGGCTTGACATCAGGGTCTATGTTTAAGTCTT 120 0; Gaps 61 GCCCAGCGCTGAGGCTGCACTTTTCCGAGGCCTTGACATCAGGGTCTATGTTTAAGTCTT GGTGGGGCCCCAGCTGAAGGAGGGAACTGAGACCCCACCAGAAGCCTCCAGAGCTGTG 1 GAATTCCGGCCTGCTGCCGGGCCGCCCCGCCCGGGCCACACGGCAGAGCCGCCTGAA 121 AGCTCTTGCTTACAAAGACCACGGCAATTCCTTCTCTGAAGCCCTCGCAGCCCCACAGGG CCCTCGCAGCCCCAGCCTGCCGCCTACTGCCCAGCAATGCCCTCCAGCGGCCCCGGGGAC 481 GACTITGGAGAAGCGGAGTGAACCCCAACCTGAGGAAGGGAGCCCAGCTGCAGGGCAGAAG 121 AGCTCTTGCTTACAAAGACCACGGCAATTCCTTCTCTGAAGCCCTCGCAGCCCCACAGCG CCCTCGCAGCCCCAGCCTGCCGCCTACTGCCCAATGCCCTCCAGCGGCCCCCGGGGAC AACCGTGGCAAGGAAGAGCGCCAGGAGCCCAAGCGCCCACGGCCCGGAAGGTGGGGAAGGCCT ACCGTGGCAAGGAAGAGCGCCAGGAGCCCAGGCCCACGCCCCGGAAGGTGGGGAGGCCC GGCCGGAAGCGCAAGCACCCACCGGTGGAAAGCAGTGACACCCCCCAAGGACCCCAGCAGTG **ACCACCAAGTCTCAGCCCATGGCCCAAGGACTCTGGCCCCTCAGATCTGCTACCCAATGGA** GACTTGGAGAAGCGGAGTGAACCCCAACCTGAGGAGGGGAGCCCCAGCTGCAGGGCAGAAG Query Match 99.7%; Score 4181.4; DB 21; Length 4192; Best Local Similarity 99.9%; Pred. No. 0; Matches 4186; Conservative 0; Mismatches 6; Indels 0; C Query Match 181 181 241 241 301 301 361 421 421 481 541 q g 8 6 8 දු ද ò ò ે a ò 유 ò q ò ò

1080 1080 1140 1200 1200 1260 1260 1320 1440 1500 1680 780 541 GGTGGGGCCCCAGCTGAAGGAGAGAACTGAGACCCCACCAGAAGCCTCCAGAGGCTGTG 600 961 CCTGCTTCTCCGACTGTGGCCACCACCCCTGAGCCAGTAGGAGGGGATGCTGGGGGACAAG CCAGCCAAGAAACCCAGAAAGAGCACAACAGAGAAACCTAAGGTCAAGGAGAGTCATTGAT GAGGCTGAGAAGAAGCCAAGGTAATTGCAGTAATGAATGCTGTGGAAGAGGAACCAGGCC GGAGAGCTGGTGTGGGGGAAACTTCGGGGTTTCTCTTGGTGGCCAGGCCGAATTGTGTGTCT 1201 GAIGGCAAGTICTCAGTGGTGTGTGTGGAGAAGCTCATGCCGCTGAGCTCCTTCTGCAGT GCATTCCACCAGGCCACCTACAACAAGCAGCCCATGTACCGCAAAGCCATCTACGAAGTC CTCCAGGTGGCCAGCAGCCGTGCCGGGAAGCTGTTTCCAGCTTGCCATGACAGTGATGAA GGCTTCCAGCCCTCGGGTCCTAAGGGCCTGGAGCCACCAGAAGAAGAAGAATCCTTAC 1441 GGCTTCCAGCCCTCGGGTCCTAAGGGCCTGGAGCCACCAGAAGAAGAAGAAGAATCCTTAC 601 GAGAATGGCTGCTGTGTGACCAAGGAAGGCCGTGGAGCCTCTGCAGGAGGGGCAAAGAA CAGAAGCAGACCAACATCGAATCCATGAAAATGGAGGGTCCCCGGGGCCGACTGCGAGGT CCTGCTTCTCCGACTGTGGCCACCACCCCTGAGCCAGTAGGAGGGGATGCTGGGGACAAG 1021 AATGCTACCAAAGCAGCCGACGATGAGCCTGAGTATGAGGATGGCCGGGGGCTTTGGCATT GATGGCAAGTTCTCAGTGGTGTGTGTGTGAAAGCTCATGCCGCTGAGCTCCTTCTGCAGT 1261 GCATTCCACCAGGCCACCTACAACAAGCAGCCCATGTACCGCAAAGCCATCTACGAAGTC 1381 AGTGACAGTGGCAAGGCTGTGGAAGTGCAGAACAAGCAGATGATTGAATGGGCCCTCGGT AAGGAAGTTTACACCGACATGTGGGTGGAGCCTGAAGCAGCTGCTTACGCCCCCACCCCCA GGCTTGGGCTGGGAGTCCAGCCTCCGTCAGCGACCCATGCCAAGACTCACCTTCCAGGCA GGAGAGCTGGTGTGGGGGAAACTTCGGGGCTTCTCCTGGTGGCCAGGCCGAATTGTGTGTCT 199 781 841 961 1141 1201 1261 1321 1321 1441 1501 1501 1561 1561 1621 1621 721 901 8 셤 ò 8 8 a y g ò g ò 8 6 8 6 8 6 8 6 8 6 8 ò 셤 ò a ò g ò q ò ò

2760 2760	2701 ATTACCACCAGGTCAAACTCTATAAAGCAGGGCAAAGACCAGCATTTCCCCCGTCTTCATG	සි
2700 2700	2641 CTGGAGCTGCAAGAGTGTCTGGAGCACGGCAGAATAGCCAAGTTCAGCAAAGTGAGGACC	ρ δ
2640 2640	2581 TACTTCTGGGGTAACCTTCCTGGCATGAACAGGCCTTTGGCATCCACTGTGAATGATAAG	당 성
2580 2580	2521 CTTGAGTCTAACCCCGTGATGATTGACGCCAAAGAAGTGTCTGCTGCACACAGGGCCCGT	Db Qy
2520 2520	GTTAGTGACAAG GTTAGTGACAAG	g Q
2460 2460		D Q
2400	2341 CTCTCCATTGTCAACCCTGCCCGCAAGGGACTTTATGAGGGTACTGGCCGCCTCTTCTTT	
2340 2340	2281 AAGCATATCCAGGAGTGGGGCCCATTCGACCTGGTGATTGGAGGCAGTCCCTGCAATGAC	p Q
2280 2280	2221 GGCATGGTGCGGCACCAGGGAAAGATCATGTACGTCGGGGACGTCCGCAGCGTCACACAG	P Q
2220 2220	2161 CTGGGCATCCAAGTGGACCGCTACATTGCCTCCGAGGTGTGTGAGGACTCCATCACGGTG	문왕
2160 2160	.01 CCCATCCGCGTGCTGTCTC	당 왕
2100	2041 CATGACCAGGAATTTGACCCCCCAAAGGTTTACCCACCTGTGCCAGCTGAGAAGAGGAAG	유 성
2040	ğ—ğ	B &
1980 1980	1921 CAGGCAGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCATAAGGGCACCTAT	
1920 1920	1861 AACTGCTGCAGGTGCTTTTGTGTCGAGTGTGTGGATCTCTTGGTGGGGCCAGGAGCTGCT	Db Qy
1860	1801 TACCAGTCCTATTGCACCATCTGCTGTGGGGGGGGGGTGAAGTGCTCATGTGTGGGAACAAC	P 9
1800	1741 ATGTGCCAGAACTGTAAGAACTGCTTCTTGGAGTGTGCTTACCAGTATGACGACGATGGG	용 성
1740 1740	GAGCCTCA GAGCCTCA	B &

T 3900	CAGGATGGGGAGAGGGAGCAGCTGGAGGGGGTTTTAACAAACTGAAGGATGACCCCATA		9
C 3840	GCAAAGACATCAGCTTCCGCCTGGGCCCTCTGTGCAAAGGGTTTCAGC	3781	Дb
	CAGCGAGATGAGCAAAGACATCAGCTTCCGCCTGGGCCCTCTGTGCAAAGGGTTTCAGC		Ş
A 3780	TATATATAAAAGGTACTGTTAACTGTACATCCCGACTTCATAATGGTGCTT		ДD
	TATATAAAAGGTACTGTTAACTGCTACATCCCGACTTCATAATGGTGCT		S
372		3661	da .
T 37	CTAGAAGCCGCTGTTACCTCTTGTTTACAGTTTATATATA		δ.
T 366	TTCAGGTGCCTACCACACAGGAAACCTTGAAGAAAACCAGT	3601	망
T 366	ACACTTTCTACAGTATTTCAGGTGCCTACCACAGGAAAACCTTGAAGAAAACCAGT	o	9
<u>ი</u> — ი	CAGGGCGCTGAGAGAACACCACAC 	3541	B 6
C 354	TAGAGACCCTCGGAGGCAGAGTCTCCTCTCCCACCCCCGAGCAGTCTCAACAGCAC	3481	Дb
C 35	AATAGAGACCCTCGGAGGCAGAGTCTCCTCTCCCACCCCCCGGAGCAGTCTCAACAGCAC	3481	٥ و
34	TTCTATATATCTCTTTGGTTGTCTCTAGCCTGATCAGATAGGAGCACAAACAGGAAGA	3421	gg
- G - 34	TATATATCTCTTTGGTTGTCTCTAGCCTGATCAGATAGGAGCACAAACAGGAAGA	4.	Ş
υ u	AGAGGGAAAATTCTATAAAAACTTAAAATATTGGTTTTTTTT	3361	рь
T 34	AAAGGGAGAGAGGGAAAATTCTATAAAAACTTAAAATATTGGTTTTTTTT	3361	Q Q
G 3360	AGAGTTATTGCAGCAAAATCAGTAACAACAAAAAGTAGAAATGCCTTGGAG	3301	Db
υ G	CAAGAGAGTTATTGCAGCAAAATCAGTAACAACAAAAAGTAGAAATGCCTTTGC	3301	ş
G 330		3241	Db
w	TTCTACTCTTTTTCAGAGGGGTTTTTCTGTTTTGTTTTG	3241	γQ
324	CCTCCCCTTC	18	Дb
w	GCAAAATAGGCCCCTCCCCTTCTTCCCCTCCGGTCCTAGGAGGCGAAC	3181	Ş
A 31		3121	рь
31	AAAAGGGTTGGACATCATCTCCTGAGTTTTCAATGTTAACCTTCAGTCCTATCT	3121	Ş
C 31	AAAAAGGAATTTAAAGCAAACCACAGAGGAGGAAAACGCCGGAGGGCTTGG	90	뮹
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C 30		3001	υЬ
	aacaaaacaaaaaaaaaacaccaagaacgaggacggagaaaagttcagcac	3001	Ş
C 3000	AAGGGACATGGGGCAAACTGAAGTAGTGATAAAAAAGTTAAACAAAC	2941	ы
C 3000	AAGGGACATGGGGGCAAACTGAAGTAGTGATGATAAAAAAGTTAAACAAAC	2941	Ş
G 2940	CGTGCCGGTCATCCGCTCTTCGCTCCGCTGAAGGAATATTTTGCTTGTGT	2881	ъ
-Q N	GAAGCGTGCCGGTCATCCGCCACCTCTTCGCTCCGCTGAAGGAATATTTTGCTTGTGT	2881	γQ
1 13 2880	ACAGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGATC	8	망
-G 28	ACTACACAGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGATC	2821	Ş
C 28		~	Db
C 2820	ACGAGAAGGAGACATCCTGTGGTGCACTGAAATGGAAAGGGTGTTTTGGCTTTCCCCGT	2761	8

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The present sequence encodes a human de novo DNA cytosine methyltransferase designated DNWT3A. The polypeptides can be administered therapeutically, especially by expressing encoding polynucleotides, to treat diseases associated with DNA cytosine methyltransferase, such as neoplastic disorders e.g. carcinomas, sarcomas and leukemias. They can be used to diagnose, or determine susceptibility to neoplastic disorders, by assaying for polypeptide expression levels in mammalian cells/body
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De novo DNA cytosine methyltransferase; DNMT3A; neoplastic disorder; carcinoma; sarcoma; leukaemia; DNA methylation; ss.
                                         3901 CACCCCCCACCCCTGCCCTGCCTAGCTTCACCTGCCAAAAAGGGGGTCAGCTGAGGTG
                                                                                                     GTCGGACCCTGGGGAAGCTGAGTGTGGAATTTATCCAGACTCGCGTGCAATAACCTTAGA
                                                                                                                                                                                                         GAATTCGTCAGCCACGTTGAAGGCCCCTTGTGGGATCAGAAATATTCCAGAGTGAGGGAA
                                                                                                                                                                                                                              4081 GAATTCGTCAGCCACGTTGAAGGCCCCTTGTGGGGATCAGAAATATTCCAGAGTGAGGGAA
                           CACCCCCCACCCTGCCCCATGCCTAGCTTCACCTGCCAAAAAGGGGGCTCAGCTGAGGTG
                                                                                                                                                                            4021 ATATGAATCTAAAATGACTGCCTCAGAAAAATGGCTTGAGAAAACATTGTCCCTGATTTT
                                                                                      GTCGGACCCTGGGGAAGCTGAGTGTGCAATTTATCCAGACTCGCGTGCAATAACCTTAGA
                                                                                                                                               ATATGAATCTAAAATGACTGCCTCAGAAAATGGCTTGAGAAAACATTGTCCCTGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "de novo DNA cytosine methyltransferase DNMT3A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
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                                                                                                                                                                                                                                                                                     4141 AGTGACCCGCCATTAACCCCCNCCTGGAGCAAATAAAAAAACATACAAAATGT 4192
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fluids. They are useful to screen for compounds inhibiting/activating the polypeptide. The polypeptides can also be used for in vitro de novo methylation of DNA. Such in vitro methylation may be used to direct or regulate DNA expression in biological systems, e.g. recombinant DNA methylated in vitro may be introduced into a cell/organism to increase or decrease expression of a desired polypeptide for which the native DNA is under-methylated or not methylated. The polypeptides can also be used to produce antibodies which are useful to detect and purify the polymocleotides are useful to produce probes and sischers. The useful diagnostically.
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                                                                                                                                                                                                                                 Query Match 68.5%; Score 2871.8; DB 21; Length 4416; Best Local Similarity 83.7%; Pred. No. 0; Matches 3574; Conservative 0; Mismatches 583; Indels 113; C
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· }	1797 TGGGTACCAGTCCTATTGCACCATCTGCTGTGGGGGGGCCTGAAGTGCTCATGTGTGGGAA 1856	유 성
S B 7	1737 AGGCATGTGCCAGAACTGTAAGAACTGCTTCTTGGAGTGTGCCTTACCAGTATGACGACGA 1796	유 성
\$ B &	1677 GGACATTTGTATCTCATGTGGGAGCCTCAATGTCACCCTGGAGCACCCACTCTTCATTGG 1736	ß 8
₽ \$ \$	1617 TGATGAGCGCACAAGGGAGCGGCTGGTGTATGAGGTGCGCCAGAAGTGCAGAAACATCGA 1676	B 8
5 B 5	1557 CCCACCAGCCAGAAAACCCCAGAAAGAGCACAACAGAGAAACCTAAGGTCAAGGAGATCAT 1616	음 성
5 B &	1497 TTACAAGGAAGTTTACACCGACATGTGGGGTGGAGCCTGAAGCAGCTGCTTACGCCCCACC 1556	
S B &	1437 CGGTGGCTTCCAGCCCTCGGGTCCTAAGGGCCTGGAGCCACCAGAAGAAGAAGAAGAATCC 1496	유 성
S B 7	1377 TGAAAGTGACAGTGGCAAGGCTGTGGAAGTGCAGAACAAGCAGATGATTGAATGGGCCCT 1436	8 8
Q	1317 AGTCCTCCAGGTGGCCAGCAGCCGTGCCGGGAAGCTGTTTCCAGCTTGCCATGACAGTGA 1376	유 성
S B 7	1257 CAGTGCATTCCACCAGGCCACCTACAACAAGCAGCCCATGTACCGCAAAGCCATCTACGA 1316	gg Qy
S B &	1197 CGGAGATGGCAAGTTCTCAGTGGTGTGTGTGGAGAAGCTCATGCCGCTGAGCTCCTTCTG 1256	용 성
S B &	1137 GTCTTGGTGGATGACAGGCCGAGCCGAGCAGCTGAAGGCACTCGCTGGGTCATGTGGTT 1196	유 성
5 B &	1077 CATTGGAGAGCTGGTGGGGGAAACTTCGGGGCCTTCTCCTGGTGGCCAAGTCGAATTGT 1136	g
Q	1017 CAAGAATGCTACCAAAGCAGCCGACGATGAGCCTGAGTATGAGGATGGCCGGGGCTTTGG 1076	\$ Q
5 B &	957 GGACCCTGCTTCTCCGACTGTGGCCACCACCCCTGAGCCAGTAGGAGGGGATGCTGGGGA 1016	유 성
S B &	897 GGCCTCTGGAGAGGTCTCAGAAGGTGGAGGAGGCCAGCCCTCCTGCTGTGTGCAGCAGCCCAC 956	유 성
}	837 AAGGGAGGCTGAGAAGAAAGCCAAGGTAATTGCAGTAATGATGCTGTGGAAGAGAACCA 896	유 성

	Db 2665 ATTTCTCGAGTCCAACCTGTGATTGATGACAGGCCTTTGGCATCACCTGTGAATGA 26 Oy 2577 CCGTTACTTCTGGGGTAACCTTCCTGGCATGAACAGGCCTTTGGCATCCACTGTGAATGA 26 Db 2725 CCGCTACTTCTGGGGTAACCTTCCCGGTATGAACAGGCCTTTGGCATCACTGTGAATGA 27 Oy 2637 TAAGCTGGAGCTGCAAGAGTGTCTGGGAGCAGGAATAGCCAAGTTCAGCAAAGTGAG 26 Oy 2637 TAAGCTGGAGCTGCAAGAGTGTCTGGAGCAGGAATAGCCAAGTTCAGCAAAGTGAG 26 Oy 2637 GACCATTACCACCAGGTCAAACTCTGATAAAGCAGGGCAAAGTCCAGCAAAGTGAG 28 Oy 2637 GACCATTACCACCAGGTCAAACTCTATAAAGCAGGGCAAAGCCAGCATTTCCCCCGTCTT 27 Db 2845 GACCATTACTACGAGGTCAAACTCCTATAAAGCAGGGCAAAAGACCAGCATTTTCCTCTCTT 27 Oy 2757 CATGAACGAGAGGACATCCTGTGGTGCACAAGAACGAGGTTTTGCCTCTT 29 Oy 2757 CATGAACGAGAGGACATCCTGTGGTGTGCAAAGGACCAAGGATTTTCCTCTCTT 29 Oy 2757 CATGAACGAGAGGACATCCTGTGGTGTGAAAGGACCAAGCATTTTCCTCTCTT 29 OY 2757 CATGAACGAGAGGACATCCTGTGGTGTGCACTGAAATGGAAAGGGTGTTTGCCCC 28	2277 2425 2337 2485 2485 2545 2545 2605	2097 2245 2157 2305 2217 2365	1917 TGCTCAGGCAGCCATTAAGGAAGACCCCTGGAACTGCT.
		ACCTGGTAATTGGAGGCAGTCCCTGCAA [GATTGCTACAGGGCTCCTGGTGCTGAA	ATGTGCGGGCATAAC ATGTGCGGGCACAAC ATGTGCGGGCACTT CTCCAGATGTTCTT CTCCAGATGTTCTTCTT CTCCAGATGTTCTTCTTCCCCAGCTGAC
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3196 GCACCCAGAAGAGAAAAAGGAATTTAAAACAAAAACCACAGAGGGGGAAATACCGGAGGG 3255
                                                                                                                                        CTATCTAAAAAGCAAAATAGGC-CCCTCCCCTTCCCCCT---CCGGTCCTAGGAGGCG 3229
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                                                                                        3114 GCTTGGCCTTGCAAAAGGGTTGGACATCATCTCCTGAGTTTTCAATGTTAACCTTCAGTC
                                                                                                           3256 CTTGCCTTGCGAAAAGGTTGGACATCATCTCCTGATTTTTCAATGTATTCTTCAGTC
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; antionvulsant; antidacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiavascular disorder; neurological disease; infection; human; secreted protein; gene; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions useful for preventing, treating or ameliorating redical conditions useful for preventing, the genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic ansemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isohamias;
                                                                                                                                               (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                 4270 TCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGAGGGCTCCTTGTGGTGGGATCAGAAC 4329
4210 TAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCTCGGCAAGATGGCAGAGGGTACGGAG 4269
                                        4063 AACATTGTCCCTGATTTTGAATTCGTCAGCCACGTTGAAGGCCCCTTGTGGGATCAGAAA 4122
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The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders -
                                                                                                                         4123 TATTCCAGAGTGAGGGAAAGTGACCCGCCATTAACCCCCNCCTGGAGCAAATAAAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 953; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 953.
                                                                                                                                                                                                                                                                                                                                                        ABL90391 standard; cDNA; 2938
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P-PSDB; ABB89982.
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Qy 2406 CTACCGCCTCCTGCATGATGCGCGGCCC	Qy 2346 CATTGTCAACCCTGCCCGCAAGGGACTT	Qy 2286 TATCCAGGAGTGGGGCCCATTCGACCTC	2226 789	2166 729	2106 669	Db 609 CCAGGAAITTGACCCCCAAAGGTITAC	Qy 1986 GCTGCGAAGACGGGAAGACTGGCCTTCT	1926 489	Qy 1866 CTGCAGGTGCTTTTGTGTCGAGTGTGTG	1806	Qy 1746 CCAGAACTGTAAGAACTGCTTCTTGGAG	Oy 1686 TATCTCATGTGGGAGCCTCAATGTCACC	Cy 1626 CACAAGGGAGCGGCTGGTGTATGAGGTG	1566 129	1506	Qy 1446 CCAGCCTCGGGTCCTAAGGGCCTGGAG	Query Match 43.3%; Scor Best Local Similarity 82.5%; Pred Matches 2327; Conservative 5; M	XX SQ Sequence 2938 BP; 759 A; 695 C; 7
CTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGAGGATGATCGCCCCTTCTTCTGGCT 2465	CATTGTCAACCCTGCCCGCAAGGGACTTTATGAGGGTACTGGCCGCCTCTTCTTTGAGTT 2405	TATCCAGGAGTGGGGCCCATTCGACCTGGTGATTGGAGGCAGTCCCTGCAATGACCTCTC 2345	∞ №	7 2	7 2		GCTGCGAAGACGGGAAGACTGGCCTTCTCGACTCCAGATGTTCTTTGCCAATAACCATGA 2045	tn 🛏	CTGCAGGTGCTTTTGTGTCGAGTGTGGGATCTCTTGGTGGGGCCAGGAGCTGCTCAGGC 1925	4	CCAGAACTGTAAGAACTGCTTCTTGGAGTGTGCTTACCAGTATGACGACGATGGGTACCA 1805	TATCTCATGTGGGAGCCTCAATGTCACCCTGGAGCACCCACTCTTCATTGGAGGCATGTG 1745	CACAAGGGAGCGGCTGGTGTATGAGGTGCGCCAGAAGTGCAGAAACATCGAGGACATTTG 1685	CAAGAAACCCAGAAAGAGACAACAGAGAAACCTAAGGTCAAGGAGATCATTGATGAGGG 1625	~ ~	AAGAGAAGAATCCTTACAAGGA 1505	Score 1814; DB 24; Length 2938; Pred. No. 0; 5; Mismatches 398; Indels 89; Gaps 19;	74 G; 700 T; 10 other;
- OY	dg dy	da cy	D CY	da 40	Db Oy	Qy	dg Qy	B &	QQ VQ	문 &	B 65	B 8	B 8	Db Qy	dg VQ	45 45	B 6	Db
/ 3436 TTGGTTGTCTCTAGCCTGATCAGATAGGAGCACAAACAGGAAGAGAATAGAGACCCTC 3493	3409 TTTTTTTCCTTTTCTATATATCTCTT	358 GAGGAAAGGGAGAGAGGGAAAATTCTATAAAAACTAAAATTTGGTTTTT 	3299 TGAAACAAGAGAGTTATTGCAGC-AAAAATCAGTAACAACAACAAGTAGAAAATGCCTTGGA	3239 TITTCTACTCTTTTTCAGAGGGGTTTTCTGTTTGTTTGGGTTTTTGTTTCTTGCTGTGAC 3298	7 3183 AAGCAAAATAGGC-CCCTCCCCCTTCTTCCCCTCCGGTCCTAGGAGGCGAACTTTTTG 3238	7 3123 TGCAAAAGGGTTGGACATCATCTCCTGAGTTTTCAATGTTAACCTTCAGTCCTATCTAAA 3182	7 3065 AGAGAAAAGGAATTTAAAGCAAACCACAGAGGAGGAAAAACGCCGGAGGGCTTGGCCT 3122 	3006 ACAAAACAAAACAATAAAACACCAAGAACGAGAAGGACGAGAAAAGT-TCAGCACCCAGA	/ 2946 GACATGGGGGCAAACTGAAGTAGTGATGATAAAAAGTTAAACAAAC	2886 1449	7 2826 CACAGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGATCGTGGAG 2885	2766 GAAGGAGGACATCCTGTGGTGCACTGAAATGGAAAGGGTGTTTGGCTTCCCCGTCCACTA	⊬ 2	H N	ري سر	7 2526 GTCTAACCCCGTGATGATTGACGCCAAAGAAGTGTCTGCTGCACACAGGGCCCGTTACTT 2585	7 2466 CTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCGCGATTTCTTGA 2525	969 CTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGGAGGATGATCGCCCCTTCTTCTGGCT

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              2098 TCAGGCGCACATTTCCCTCCCAGCCACTGAGCTGTCGTGCCAGCACCATTCCTGGTCAC 2157
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3494 GGAGGCAG-AGTCTCCTCTCCCCCCCCGAGCAGTCTCAACAGCACCATTCCTGGTCAT 3552
                                                                                                                                                                                                                               2335 GGTACTGTTAACTGTACAACCCGACTTCATAATGGTGCTTTC-AAACAGCGAGATGA 2393
                                                                                                                                                                                                                                                         GCAAAGACATCAGCTTCCGCCTGGCCCTCTGCAAAGGGTTTCAGCCCAGGATGGGGAG 3852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2217 CAGTATTTCAGGTGCCTACCACACACAGAAACCTTGAAGAAAATCAGTTTCTAGAAGCCGC
                                                                                                                                                     GGTACTGTTAACTACTGTACATCCCGACTTCATAATGGTGCTTTCAAAACAGCGAGATGA
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                                                  DNA encoding de novo DNA cytosine methyltransferase Dnmt3bl.
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The present sequence encodes a murine de novo DNA cytosine methyltransferase designated Dmmt3b. The Dmmt3b gene also produces, through alternate splicing, at least two shorter isoforms of 840 and through alternate splicing, at least two shorter isoforms of 840 and 77 amino acid residues, termed Dmmt3b2 and Dmmt3b3 (sequences or through alternate splicing, expecification). The polypoptides can be administered to the appearizally, especification). The polypoptides can be administered the respectively, especification). The polypoptides can early laransferase, such as neoplastic disorders, or determine susceptibility to neoplastic disorders, by assaying for polypoptide expression levels in mammalian cells/body [10] polypoptide. The polypoptide expression levels in mammalian cells/body connethylation of DNA. Such in vitro mathylation may be used for in vitro de novo methylation of DNA. Such in vitro methylation may be used to direct or regulate DNA expression in biological systems, e.g. recombinant DNA methylated in vitro may be introduced into a cell/organism to increase or decrease expression of a desired polypoptide can also be used to produce antibodies which are useful to detect and purify the polypoptide or therapeutically e.g. to treat neoplastic disorders. The polypoptide are useful to produce probes and primers which are useful diagnostically.
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18.1%; Score 757.8; DB 21; Length 4195;
Best Local Similarity 63.4%; Pred. No. 4.7e-174;
Matches 1250; Conservative 0; Mismatches 702; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                    New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
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                                                                                           98US-0090906.
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                        CGCCTCCTGCATGATGCGCGGCCCAAGGAGGGAGATGATCGCCCCTTCTTCTGGCTCTTT
                                                                                                          GTCAACCCTGCCCGCAAGGGACTTTATGAGGGTACTGGCCGCCTCTTCTTTGAGTTCTAC
                                                                                                                                                                    GAAGAGTGGGGCCCGTTCGACTTGGTGATTGGTGGAAGCCCATGCAATGATCTCTCTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De novo DNA cytosine methyltransferase; DNMT3B1; neoplastic disorder;
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New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
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                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-106298/09.
P-PSDB; AAYS4058.
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24-JUL-1998;
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contributions designated DNMT3B1. The DNMT3B gene also produces, through alternate splicing, at least two shorter isoforms termed DNMT3B2 (comprising amino acids 1-355 and 376-853 of AAY54059, see AAY54059) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 of AAY54059) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 of AAY54059, see AAY54060) (sequences not given in the specification).

CAAY54059 and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 of AAY54059, see AAY54060) (sequences not given in the specification).

CAAY54059 and DNMT3B3 (comprising the polypecially by expressing encoding polymucleotides, to treat diseases associated with DNA cytosine methyltatransferase, such as neoplastic disorders e.g. carcinomas, sarcomas and leukemias. They can be used to disorders e.g. carcinomas, sarcomas and leukemias. They can be used to disorders in the compounds inhabiting/activating the polypeptide. The polypeptides can also be used for in vitro de nevo methylation of DNA.

Such in vitro methylation may be used to direct or regulate DNA.

Such in vitro methylation may be used for in vitro de nevo methylation of Corpora in biological systems, e.g. recombinant DNA methylated in vitro may be used to direct or regulate DNA.

Such in vitro methylated or not methylated. The polypeptides can also be used to produce antibodies which are useful to detect and purify the polypeptide corporate and primers which are useful
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Query Match Best Local Similarity

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Length

Sequence 709

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                         AB056306 to AB060787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the AB060787 to AB060787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide for detecting the presence or absence of a polymucleotide encoded by a for detecting the presence or absence of a polymucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the presence of cells in a sample of cells from a patient. (I) is useful for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                         Claim
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AAH32943 to AAH37195 and AAG73514 to AAG7778B represent human colon cancer associated nucleic acid molecules (N) and proceedins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene cancer antigens have cytostatic activity and can be used in the prevention. Color cancer antigens have cytostatic activity and can be used in the prevention, changes associated with inappropriate P prevention. N and P may be used in the prevention.

CC diagnosis and treatment of diseases associated with inappropriate P color cancer associated with decreased expression by exectifying mutations or deletions are proteins or to supplement the patients own production of P color cancer associated Ps.

CC Additionally, N may be used to produce the colon cancer-associated Ps.

CC Additionally, N may be used to produce the colon cancer-associated Ps.

CC Additionally, N and be cards into a host cell and culturing the color cancer associated Ps.

CC Additionally, N and cards into a best cell and culturing the color cancer associated Ps.

CC Additionally, N and processor actis into a best cell and culturing the color cancer associated Ps.

CC Additionally, N and processor actis into a best cell and culturing the color cancer associated Ps.

CC Additionally, N and page 7003 of the sequence listing were concerned by the color cancer associated Ps.

CC Missing at time of publication, meaning no sequences are present for concerned processor.
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                                                                                                                                                   Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1970 AGGGCACCTATGGGCTGCTGCGAAGACGGGAAGACTGGCCTTCTCGACTCCAGATGTTCT 2029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 ACATCACAAAGAAAAATATTGAAGAATGGGGCCCATTTGACTTGGTGATTGGCGGAAGCC 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 CCATTGCTGTTTGGAACCGTGAAGAGAGGGAATATCAAATACGTGAACGAYGTGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2270 GCGTCACACAGAAGCATATCCAGGAGTGGGGCCCCATTCGACCTGGTGATTGGAGGCAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1060 BP; 267 A; 262 C; 297 G; 227 T; 7 other;
                                                                    Rosen CA;
                                                                                                                                                                                                         Claim 1; Page 2829; 9803pp; English.
                                                                    Birse CE,
                                  (HUMA-) HUMAN GENOME SCI INC.
99US-0163280.
                                                                    Ruben SM, Barash SC,
                                                                                                         WPI; 2001-235357/24.
03-NOV-1999;
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                                                                                                      2310 CCTGGTGATTGGAGGCAGTCCCTGCAATGACCTCTCCATTGTCAACCCTGCCGCAAGGG 2369
                                                                                                                                                                             2370 ACTITATGAGGGTACTGGCCGCCTCTTTGAGTTCTACCGCCTCCTGCATGATGCGCG 2429
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                                                                                                                                                                                                                                                                                                                  2490 CGTTAGTGACAAGAGGACATCTCGCGATTTCTTGAGTCTAACCCCGTGATGATTGACGC 2549
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                                      2250 GTACGTCGGGGACGTCCGCAGCGCTCACAGAAGCATATCCAGGAGTGGGGGCCCATTCGA 2309
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                                                            Gaps
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      . 9
      73; Indels
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        0; Mismatches
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        Matches 624; Conservative
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                                                                                                                                                  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
Primer sets for synthesizing polynucleotides, particularly the 5602 \text{ full-length cDNAs} defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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                                                              WPI; 2001-318749/34
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                                                                                    Isogai T,
Sugiyama
                                                                                                                                                                                                                                                                                                                                                      sequence SEQ ID NO:11099.
                                                                                                                                                ; 99JP-0248036.
; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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T, Wakama
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                                                                                    hikawa T,
Wakamatsu
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A, Nagai I
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Otsuki
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Claim 8 SEQ ü 11099; 2537pp + G ROM; English

sequence and an oligonucleotide comprising a sequence complementary to a conjunct point of the sequence, where the oligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as and any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH12742 represent human cDNA sequences; AAB92446 to AAH13633 to AAH13642 represent human cDNA sequences; AAB92446 to AAH13630 represent oligonucleotides, all of which are used in the exemplification of the present invention. The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end oligonucleotide comprises at least 15 nucleotides; or (b) a combination the 5602 nucleotide sequences defined in the specification, where the

Sequence 3017 BP; 749 A; 751 C; 760 G; 757 T; 0 other;

Query Match Best Local :

685;

Conservative

Similarity

11.5%;

Score 482.8; DB 22 Pred. No. 4.5e-107;

22;

Length

3017;

S S 밁 Ś 밁 5 밁 S 밁 Ś 밁 Ş 뮹 8 밁 Š 밁 Ś 믕 밁 Ş Matches 2157 2037 1917 1797 1737 1677 1617 2097 1977 1857 969 849 789 729 669 609 549 489 429 TGATGAGCGCACAAGGGAGCGGCTGGTGTATGAGGTGCGCCAGAAGTGCAGAAACATCGA 1676 GGTGGGCATGGTGCGGCACCAGGGAAAGATCATGTACGTCGGGGACGTCCGCAGCGTCAC GAAGCCCATCCGCGTGCTGTCTCTCTTTGATGGGATTGCTACAGGGCTCCTGGTGCTGAA GGACATTTGTATCTCATGTGGGAGCCTCAATGTCACCCTGGAGCACCCACTCTTCATTGG 1736 GGACCTGGGCATCCAAGTGGACCGCTACATTGCCTCCGAGGTGTGTGAGGACTCCATCAC TAACCATGACCAGGAATTTGACCCCCCAAAGGTTTACCCACCTGTGCCAGCTGAGAAGAG CTATGGGCTGCGAAGACGGGAAGACTGGCCTTCTCGACTCCAGATGTTCTTTGCCAA AGCGGCCGAGGCTTCAGGAGCCCTGGAGCTGCTACATGTGTCTCCCGCAGCGCTG TGCTCAGGCAGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCATAAGGGCAC 1976 TGGGTACCAGTCCTATTGCACCATCTGCTGTGGGGGGCGTGAAGTGCTCATGTGTGGGAA 1856 GGGGCTCTGTCAGACATGCCGGGATCGCTTCCTTGAGCTGTTTTACATGTATGATGACGA AGGCATGTGCCAGAACTGTAAGAACTGCTTCTTGGAGTGTGCTTACCAGTATGACGACGA 1796 AGATEGCTETTTGTCTTGTGGCAGGAAAAACCCCGTGTCCTTCCACCCTCTCTTTGAGGG TGAAGATCAGAGCCGAGAACAAATGGCTTCAGATGTTGCCAACAACAAGAGCAGCCTGGA 488 ${f AGAGTTGGGCATAAAGGTAGGAAAGTACGTCGCTTCTGAAGTGTGAGGAGTCCATTGC}.$ GCGGCCCATTCGAGTCCTGTCATTGTTTGATGGCATCGCGACAGGCTACCTAGTCCTCAA TGGCACGGGGCTTGAATACGAAGCCCCCAAGCTGTACCCTGCCATACCCGCAGCCCGAAG TCATGGCGTCCTGCGGCGCCGGAAGGACTGGAACGTGCGCCTGCAGGCCTTCTTCACCAG CACGAGCTGCTGCCGGTGTTTCTGTGTGGAGTGCCTGGAGGTGCTGGTGGGCACAGGCAC CAACAACTGCTGCAGGTGCTTTTGTGTCGAGTGTGTGGATCTCTTGGTGGGGCCAGGAGC 1916 TGGCTATCAGTCTTACTGCACTGTGTGCTGCGAGGGCCGAGAGCTGCTGCTTTGCAGCAA 0 Mismatches 337; Indels 0 Gaps 2276 2216 2156 668 896 2096 2036 728 809 806 848 788 548 0

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14-AUG-2000) 2000US-0225213.

14-AUG-2000) 2000US-0225214.

14-AUG-2000) 2000US-0225267.

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14-AUG-2000) 2000US-0225267.

14-AUG-2000) 2000US-0225276.

14-AUG-2000) 2000US-022547.

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16-AUG-2000) 2000US-022547.

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16-AUG-2000) 2000US-022948.

16-SEP-2000) 2000US-022949.

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16-SEP-2000 2000US-02399.

16-SEP-2000 2000US-02399
            Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                 CTTTGAGTTCTACCGCCTCCTGCATGATGCGCGCCCAAGGAGGAGGAGATGATCGCCCCTT
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                                                                                             2277 ACAGAAGCATATCCAGGAGTGGGGCCCATTCGACCTGGTGATTGGAGGCAGTCCCTGCAA
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2000US-018628.
2000US-0186350.
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2000US-0209467.
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2000US-0216647.
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4-FEB-2000; 2
C0-MAR-2000; 2
I6-MAR-2000; 2
I1-MAR-2000; 2
I1-MAR-2000; 2
I1-MAR-2000; 2
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I1-JUL-2000; 2
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Best Local Similarity 87.7%;
Matches 471; Conservative
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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
                                       1446
                                                                                                                        The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the
1506 AGTTTACACCGACATGTGGGTGGAGCCTGAAGCAGCTGCTTACGCCCCACCCCCACCAGC 1565
                                                                                              Sequence 622
                                                                                                                                                                                                                         WPI; 2001-465570/50.
P-PSDB; AAM94301.
                                                                                                                                                                         Claim
                                                                                                                                                                                        Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                       (HUMA-) HUMAN
                     N
                                  CCAGCCCTCGGGTCCTAAGGGCCTGGAGCCACCAGAAGAAGAAGAAGAATCCTTACAAGGA 1505
                  CCAGCCTTCTGGCCCTAAGGGCCTAGAGCCACCAGAAGAAGAAGAATCCCTACAAAGA
                                                                                                                                                                     SEQ ID NO 272; 1297pp + Sequence Listing; English.
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2000US-0251868.
2000US-0251869.
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2000US-0254097.
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2000US-0249299.
2000US-0250391.
2000US-0250391.
2000US-0250391.
                                                                                              BP; 154
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                                                                                             A; 161 C; 189 G; 112 T; 6 other;
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                                                       2;
                                                       Score 413; DB 22;
Pred. No. 2.1e-90;
2; Mismatches 62;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromomomers.

chromosome

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RESULT 10
AAS86165
                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder;
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  Claim
                                                                                                                                             P-PSDB;
                                                                                                                                                                                                      Drmanac
                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding
                                          biodiversity
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                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
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                                                                                                                                           2001-639362/73.
DB; ABG21978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCATAAGGGCACCTATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAAAACTGCAAGAACTGCTTTCTGGAGTGTGCGTACCAGTACGACGACGACGGCTACCA
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1; SEQ ID No 21969; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel human diagnostic protein #21969
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and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or guarticating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating cities any polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of act and products dependent on DNA and classification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences.
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8.1%; Score 341; DB 23; Length 711;
Best Local Similarity 74.7%; Pred. No. 7.9e-73;
Matches 428; Conservative 0; Mismatches 145; Indels Conservative 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 711 BP; 181 A; 164 C; 199 G; 167 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2650 CAAGAGTGTCTGGAGCACGCCAGAATAGCCAAG 2682
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08-JUN-2001

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The present invention relates to a composition comprising several polymucleotide probes. Probes can be derived from the present sequence. The probes are immobilised and are preferably useful as hybridisable array elements in a microarray for monitoring the expression of several polymucleotides. The microarray can be used in the disgnosis of cancers such as adenocarcinoma etc., immunopathology such as AIDS, Addison's and tetratocarcinoma etc., immunopathology such as AIDS, Addison's atherosclerosis and bronchitis etc., neuropathology such as AIDS, asthma, atherosclerosis and bronchitis etc., neuropathology such as AIDS, asthma, atherosclerosis and bronchitis etc., neuropathology such as AIDS, asthma, atherosclerosis and bronchitis etc., neuropathology such as AIDS in more and cerebral neoplasms etc. The microarray can also be used to investigate an individual's predisposition to a disease such as cancer, investigating cellular response to infection, drug treatment etc. The microarray can be used for disgnostics, prognostics and treatment etc. The expanse, drug discovery and development, toxicological and carray can elso be used for monitoring disease progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition having probes which comprise part of gene sequence encoding proceins associated with cell proliferation useful as hybridizable array elements in Microarrays to monitor expression of target polymuclectide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2387 GCCGCCTCTTCTTTGAGTTCTACCGCCTCCTGCATGATGCGCGCCCCAAGGAGGAGATG 2446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GGCGGCTCTTCTTCGAATT-TTCCACCTGCTGAATTACTCACGCCCCAAGGAGGTGATG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CAAAGAATGATAAACTCGNGCTGCAGGACTGCTTGGAATACAATAGGATAGCCAAGTTAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 2077;
                                                            Probe; microarray; cancer; immunopathology; neuropathology; ss.
                                                                                                                                                                                                                                                                                                                                                                      Guegler KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.8%; Pred. No. 1.4e-00, Indels of Mismatches 139; Indels
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                                                                                                                                                                                                                                                                                                                                                                   Yue H, Reddy R,
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4.8%; Pred. No. 1.4e-68;
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                    Receptor #25 partial coding sequence.
                                                                                                                                                                                                                                                                                                                                                                   Lal P, Hillman JL,
                                                                                                                                                                                                                                     99US-0276531.
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                                                                                                         Balaena mysticetus.
                                                                                                                                                                                                                                     25-MAR-1999;
                                                                                                                                                                                                                                                                                27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                   Bandman O,
Baughn MR;
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RESULT 12
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS
                                                                                                                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                             Okubo
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                                                                                                                                                                                                                            2245pp; Japanese.
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RESULT 13
ABA20255
ID ABA20
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                       31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthrittic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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2000US-0179065.
2000US-0186628.
2000US-0184664.
2000US-01846350.
2000US-0189074.
2000US-0190076.
2000US-0190176.
2000US-025515.
2000US-0203467.
2000US-0216135.
2000US-0216135.
2000US-0216135.
2000US-0216135.
2000US-0216880.
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Pred. No. 3.9
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11-JUL-2000; 2000US-0217487.

11-JUL-2000; 2000US-0217486.

11-JUL-2000; 2000US-0217496.

14-JUL-2000; 2000US-0220963.

26-JUL-2000; 2000US-0220964.

14-AUG-2000; 2000US-0222513.

14-AUG-2000; 2000US-0225266.

14-AUG-2000; 2000US-0225266.

14-AUG-2000; 2000US-0225266.

14-AUG-2000; 2000US-0225266.

14-AUG-2000; 2000US-022526759.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225268.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-022567.

14-AUG-2000; 2000US
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20 - OCT - 2000 | 2000US - 0244221 | 10 - NOV - 2000 | 2000US - 024617 | 10 - NOV - 2000 | 2000US - 024617 | 10 - NOV - 2000 | 2000US - 024617 | 10 - NOV - 2000 | 2000US - 024617 | 10 - NOV - 2000 | 2000US - 024617 | 10 - NOV - 2000 | 2000US - 024617 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024652 | 10 - NOV - 2000 | 2000US - 024920 | 11 - NOV - 2000 | 2000US - 024920 | 11 - NOV - 2000 | 2000US - 024920 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024921 | 11 - NOV - 2000 | 2000US - 024925 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 024926 | 11 - NOV - 2000 | 2000US - 02

(HUMA-) HUMAN GENOME SCI INC

Ϋ́ Rosen CA, Barash SC,

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 12586; 1701pp + Sequence Listing; English

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB1801) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)sqonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, lung, or uroganital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

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RESULT 14
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Matches 223;
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     Claim
                                                                      New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutauresponsible for genetic disorders or other traits and to assure the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the 
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23-AUG-2000; 2000US-0649167
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DB; ABG21979.
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supplement; medical imaging; diagnostic; genetic disorder;
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CC Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cat figure in the printed specification in the printed specification in the printed specification in the printed cat figure in the printed specification in the printed specification format directly from WIPO cat figure in the printed in electronic format directly from WIPO cat figure in the printed in electronic format directly from WIPO cat figure in the printed in electronic format directly from WIPO cat figure in the printed in the printed in the printed in the printed in the printed in the printed in the printed in the printed in the printed in the printed in the printed in the printed in the printed in the printed i
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                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                                  disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia ann epilepsy; and (f) infectious diseases such as viral, bacterial, fungand parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directlifrom WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding 3224 human useful for preventing, diagnosing cancers and metastases -
                                                                                                                                                                                                                         Sequence 283
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2000US-0235484. 2000US-0235834. 2000US-0233063. 2000US-0233064. 2000US-0233065.

2000US-0234223

14-SEP-2000

2000US-0232400 2000US-0232401

2000US-0232398 2000US-0232399

2000US-0232081. 2000US-0231968. 2000US-0232397.

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141 AATGGGGACTTGGAGAAGCGGAGTGAGCCCCAGCCAGAGGAGGAGGGGAGCCCTGCTGGGGGG 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Rodent
1 (bases 1 to 4195)
Okano, M., Xie, S. and Li, E.
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Direct Submission
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/ product "PUA Cytosine-5 methyltransferase 3B1"
/protein_id="AAC40178.2"
/protein_id="AAC40178.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to EST sequences deposited in GenBank Accession Numbers AA116694, AA119979, AA177277, AA210 AA407106, and AA575617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="alternatively spliced product; contains Cys-rich region; C-terminal region is similar to corresponding region of DNA cytosine-5 methyltransferase 3A" /codon_start=1
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Ş	72:	AlaCysAsnProValMetIleAspAlaTleLysValCarry
90	2429	GCATGTAACCCAGTGATGATGCATGCATCAACCTTTTTTTT
Ş	741	
g	2489	TTCTGGGGTAACCTACCCGGAATGAACACACCCCTCATCATCCTTTATTCTTTTTTTT
8	761	
В	2549	GAGCTGCAGGACTGCAGTTCAGTAGGACGACCABAACTTTATAGAGACTGCAGGACTGCAGGACTTCAGTAGGACGACCABAACTTTAGAGACGACGACGACGACGACGACGACGACGACGACGACG
Ŷ	781	ThrThrLysSerAsnSerIleArgGlnGlvIvs&scrCl-r
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ş	801	GlyLysAspAspValLeuTrpCysThrGluLeuGluArg1; The CivilaGTCATGAAT 2668
В	2669	GCAAGGACGACTTTTGTGGTGCACTGAGCTCGAAAGGATCTTTCCCTTTTTTTT
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DЪ	2729	TACACGGACGTGTCCAACATGGGCCGCGGGGCCCCTTAGAACCTTCTTCTTTTTTTT
5	841	SerValProValIleArgHisLeupheAlaProTentValValValValValValValValValValValValValV
8	2789	AGTGTACCGGTCATCAGACACCCGGTTTGCCCCCCTTGAAGGACTACTTTAGATTATTTTTTTT
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-Q=/Ggn2 | USBTO_Spool/US09720086/runat | 18112002 | 092832 | 22195/app_query.fasta_1.4252
-DB=GenEmb1 -OFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MARIX+blosum62 -TRANS-human10.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-YGAPOF=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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SUMMARIES

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ALIGNMENTS

Pred. No.:

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Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmc3b) mRNA, alternatively spliced, complete cds.
                                                                                                                                                                                                                                                                                                                                                        Okano, M., Chijiwa, T., Sasaki, H. and Li, E.
Direct Submission
Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327979.
                                                                                                                                                                                                                                                                             2 (bases 1 to 4195)
Xie,S., Okano,M. and Li,E.
Direct Submission
Submitted (28-MAY-1998) CYRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, Wan 02129, USA
3 (bases 1 to 4195)
                                                                                                                         Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 4195)
0 (kano, M. Xie, S. and Li, E.
Cloning and characterization of a family of novel mammalian DNA
(cycosine-5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
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/gene="Dimt3b"
/note="similar to EST sequences deposited in GenBank
Accession Numbers AA116694, AA119979, AA17277, AA210568,
269. .2848
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/note="alternatively spliced product; contains Cys-rich
region; C-terminal region is similar to corresponding
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/codon start=1
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/chromosome="2"
/map="84.0 cM"
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Alignment Scores:

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                                                                                                                                                          Shen,Y.

Direct Submission

Submitted (17-MAY-1999) Department of Biochemistry and Molecular Submitted (17-MAY-1999) Medical Sciences, Chinese Academy (Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae,
1 (bases 1 to 4223)
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Mus musculus DNA cytosine-specific
(Dnmt3b) mRNA, complete cds.
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Yin, B., Chen, Y.T., Zhu, M.,
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                                          /gene="Dnmt3b"
297. .2876
/gene="Dnmt3b"
/function="methylates
/note="alternatively ;
                                                                /db_xref="taxon:10000"
/dev_stage="8-9 day ol
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Mismatches:
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දි සි	441	441 LeuSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCys 460
ò	461	GlnSerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAspGlyTyrGln 480
요 :	1792	CAGAGTIGCCGGGATCGCTTCCTAGAGCTCTTCTACATGTATGATGAGGAGGGCTATCAG 1851
දු දු	1852	SELTATION OF THE STATE OF THE S
à	501	CysArgCysPheCysValGluCysLeuGluValLeuValGlyAlaGlyThrAlaGluAsp 520
8 8	1912	Tecasalectricisterseasoristriceaseterreseasoricasoricasoricasoriasoriasoriasoriasoriasoriasoriasori
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ò	541	LeuargargarghygaspTrpAsnMetArgLeuGlnaspPhePheThrThrAspProAsp 560
qa	2032	CTCCGACGCAGGAAAGATTGGAACATGCGCTGCAAGACTTCTTCACTACTGATCCTGAC 2091
ò	561	
g G	2092	CTGGAAGAATTTGAGCCACCCAAGTTGTACCCAGCAATTCCTGCAGCCAAAAGGAGGCCC 2151
ò	581	IleArgValLeuSerLeuPheAspGlyIleAlaThrGlyTyrLeuValLeuLy8GluLeu 600
g	2152	ATTAGAGTCCTGTCTCTGTTTGATGGAATTGCAACGGGGTACTTGGTGCTCAAGGAGTTG 2211
ò	601	GlylleLysValGluLysTyrIleAlaSerGluValCysAlaGluSerIleAlaValGly 620
g	2212	GGTATTAAAGTGGAAAAGTACATTGCCTCCGAAGTCTGTGCAGAGTCCATCGCTGTGGGA 2271
δ	621	ThrvallysHisGluGlyGlnIleLysTyrValAsnAspValArgLysIleThrLysLys 640
qq	2272	ACTGTTAAGCATGAAGGCCAGATCAATATGTCAATGACGTCCGGAAAATCACCAAGAAA 2331
ò	641	AsnileGluGluTrpGlyProPheAspLeuValileGlyGlySerProCysAsnAspLeu 660
qq	2332	AATATIGAAGAGIGGGGCCCGTICGACTIGGTGATIGGIGGAAGCCCAIGCAATGATCTC 2391
ò	661	SerAsnValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGlu 680
QQ	2392	ictaacetcaatccieccecaaaestitatateaeeecacaeaaeectcitcticeae 2451
ò	681	PheTyrHisLeuLeuAsnTyrThrArgProLysGluGlyAspAsnArgProPhePheTrp 700
qq	2452	TITIACCACITGCTGAATTATACCCGCCCCAAGGAGGCGACAACCGTCCATTCTTCTGG 2511
à	701	MetPheGluAsnValValAlaMetLysValAsnAspLysLysAsplieSerArgPheLeu 720
q	2512	ATGTTCGAGAATGTTGTGGCCATGAAAGTGACAAGAAAAGACATCTCAAGATTCCTG 2571
ò	721	AlaCysAsnProValMetIleAspAlaIleLysValSerAlaAlaHisArgAlaArgTyr 740
дg	2572	dearchaaccaarantarcaarccarcaacarcaacarcacacacacacacacac
ò	741	PheTrpGlyAsnLeuProGlyMetAsnArgProValMetAlaSerLysAsnAspLysLeu 760
QQ	2632	Trenggggraaceraceggaargaacegggegegregaagaargaargaraacee 2691
ò	761	GluLeuGlnAspCysLeuGluPheSerArgThrAlaLysLeuLysLeuLysValGlnThrIle 780
QQ	2692	gagetigeagaktigeetiggagtteagtaggaeagaeaaagttaaagaaagtgeagaeata 2751
ò	781	ThrhrhysSerAsnSerIleArgGlnGlyLysBAsnGlnLeuPheProValValMetAsn 800
đ	2752	. Accaccaagrogaacrocatcagacagggcaaaaaccagcrirircccrgractargaar 2811

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                                                                                                                                                                                                                                                                                                                                                                   Charlestown, MA 02129, USA
Sequence update by submitter
On Nov 18, 1999 this sequence
Location/Qualifiers
1. 4135
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-NOV-1999) CVRC,
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Okano, M., Chijiwa, T., Sasaki, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charlestown, MA 02129, USA (bases 1 to 4175)
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Direct Submission
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Mammalia; Eutheria;
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Joning and characterization of a
Coytosine-5) methyltransferases
Vat. Genet. 19 (3), 219-220 (1998)
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            SRRRRASSSASTPWSSPASVDFMEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESRD
GDSTEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
SEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
                                                                                                                                       /note="alternatively spliced product; region; C-terminal region is similar tregion of DNA cytosine-5 methyltransfe
QLKPMLEWAHGGFKPTG1EGLKPNKKQPENKSRRTTNDSAASESPPPKRLKTNSYG0
                                                /translation="mKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
AICTEPVCTPETRGRRSSSRLSKREVSSLLNYTQDMTGDGDDDDDDDGNGSDILMPK
LTRETKDTRTRSESPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQBYPVEFPATR
                                                                                     /codon_start=1
/product="DNA cytosine-5
/protein_id="AAC40179.2"
/db_xref="GI:6449472"
                                                                                                                                                                                                                        AA407106,
                                                                                                                                                                                                                                  /note="similar to EST sequences deposited in GenBank
Accession Numbers AA116694, AA11979, AA177277, AA21
                                                                                                                                                                             /gene="Dnmt3b"
/function="de novo DNA methylation"
                                                                                                                                                                                                                                                          /gene="Dnmt3b"
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KDRGEDEESREMASEVTINNKGNLEDRCLSCGKKNPVSFHPLFEGGLCQSCRDRFLEL
FYMYDEDGYQSYCTVCCEGGRELLLCSNTSCCRCCFCVECLEVLVGAGTAEDAKLQEPWS
CYMCLPQRCHGVLRRRKDMNMLQDFFTTDPDLEEFEPPKLYPA, FAAKKRPIRVLSL
FDGLATGYLVLKELGIXYKEXXIASEVCLAESIAVGTVKHEGQIXYVNDVRXITKKMIEE
MGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFYHLLNYTRPKEGDNRPFFWMF
ENVVAMKVNDKKDISRFLACNPVNIDAIKVSAAHRARYEMGNLFGMNRPFWMASKXDKL
ELQDCLEFSRTAKLKKVQTITTKSNSIRQGKNQLFPVNMGKDDVLWCTELERIFGFP
ANYTDVSNNGGGARQKLLGRSWSYPVIRHLFAPLKDYFACE"

1043 a 1048 c 1106 g 938 t

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Percent Similarity:
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Query Match:
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AFIS1974 4163 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 6 (Dnnt3) mRNA, complete cds. AFIS1974 AFIS1974.1 GI:8347130
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
P.R.China
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Mammallai, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Musinae, Dases 1 (bases 1 to 4163)
Yin, B., Chen, Y. T., Zhu, M., Luo, Y. J., Zhu, N., Xu, S. C., Wu, G. Y. and
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SRRRRASSASLTPMSSPASVDFMEEVTPKSVSTBSVDLSQDGDGEMDTTQVDAESIY
GDSTEYQDDKEPGIGDLVMGKIKGFSWMPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
SEISADKLVALGLFSQHFNLATFNKLVSYRAMYHTLEKARVAGKTFSSSSPGESLED
QLKPMLEWAHGGFKPTGIEGLKENKKQPENKSRRRTTNDSAASESPEKRLKTNSYGG
KDRGEDEESRERMASEVTNNKGNLEDRTCLSCGKKNPVSFHPLFEGGLCQSCRDRFLEL
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FDGIATGYLVLKELGIKVEKYIASEVCAESIAVGTVKHEGQIKYVNDVKXITKKNIEE
WGPPDLVIGGSPCNDLSRVLAVPWIDALKTSAFFFEFFHLLNYTRPKEGDNRFFWMF
ENVJAMKVNDKKDISRFLACNEVWIDALKTVSAAHRARVFWGNLPGMNRFVMASKNDKL
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1857 CTCCGACGCAGGAAAGATTGGAACATGCGCCTGCAAGACTTCTTCACTACTGATCCTGAC 1916
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AF151970 ARNA linear ROD 08-JUN-2000 MENA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 2 (Dmm13b) mRNA, complete cds.
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
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product="DNA cytosine-specific methyltransferase isoform
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
Shen, Y.
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	Ş	1492 CAAC	Ü
2512 G	뫄	36	ફ
_	Q	1432 GAGTGGGCCCACGGTGGCTTCAAGCCTACTGGGATCGAGGGCCTCAAACCCCAAC	문
2452 A	B &	341 GluTrpAlaHisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnLysLy	Ş
	, B	7 321 GIYLYSTNENESERSERSERFROGLYGIUSERLEUGIUABPGINLEULYSBROMELLEU 340 	B 2
2332 T	& B	1312 AAGCTGGTTTCTTATAGGAAGGCCATGTACCACACTCTGGAGAAAGCCAGGGTTCGAGCT 1	D D
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2272 A	₽ 2	/ 281 AlaasplysLeuValalaLeuGlyLeuPheSerGlnHisPheAsnLeuAlaThrPheAsn 300 	당 양 양
	9 B	/ 261 AlaMetProGlyMetArgTrpValGlnTrpPheGlyAspGlyLysPheSerGluIleSer 280 1192 GCCATGCCCGGAATGCGCTGGGTACAGTGGTTTGGTGATGGCAAGTTTTCTGAGATCTCT 1251	B 성
2152 G	ον Β	1132 AAGGCTTCTCCTGGTGGCCTGCCATGGTGGTGTCCTGGAAAGCCACCTCCAAGCGACAG 1	D
601 G	Qy	1072 AGCACAC	S B
2092 A	Db 4	221 SerThrGluTyrGlnAspAspLysGluPheGlyI1eGlyAspLeuValTrpGlyLysI1e 2	; &
32	944	7 201 ASPOLYASPOLNGLUGIYMEEASPIINTTHYGLHVALASPALAGIUSETATGASPGIYASP 220 	B 5
1972 C	S B	952 GACTTCATGGAAGAAGTGACACCTAAGAGCGTCAGTACCCCATCAGTTGACTTGAGCCAG 1	рb
541 L	δ	181 AspPheMetGluGluValThrProLysSerValSerThrProSerValAspLeuSerGln 2	Ş
1912 G	Db \$	/ 161 SerArgArgArgAlaSerSerSerAlaSerThrProTrpSerSerProAlaSerVal 180 .	B 6
1852 T	S B	832 CGAGGTCGGCAGGGCCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCGGCTACCAGG 8	рb
501 C	Oy	141 ArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaThrArg 1	Ş
1792 T	Db 43	/ 121 ThrArgHisSerAsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThr 140	^무 상
	2 B	101 ProLysLeuThrArgGluThrLysAspThrArgThrArgSerGluSerProAlaValArg 120	B OY
1672 T	Q B	652 ACAGGAGATGAGAGATGATGATGATGATGGGATTGGCTCTGATATTCTAATG	₽
441 L	γo	81 ThrGlyAspGlyAspArgAspAspGluValAspAspGlyAsnGlySerAspIleLeuMet 1	ફ
1612 A	9d {}	/ 61 SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAspMet 80 .	유 성
52	B B	/ 41 ProValLeuGluAlaIleCysThrGluProValCysThrProGluThrArgGlyArgArg 60 	B 8
401 P	, vo	472 ATTATCGTTAATGGGA	망
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Qy 741 PheTrpGlyAsnLeuProGlyMetAsnArgProValMetAlaSerLysAsnAspLysLe {	Qy 721 AlacysAsnProValMetIleAspAlaIleLys	Qy 701 MetPheGluAsnValValAlaMetLysValAsn	Qy 681 PheTyrHisLeuLeuAsnTyrThrArgProLys	Qy 661 SerasnValasnProAlaArgLysGlyLeuTyrGluGlyTh	Qy 641 AsnIleGluGluTrpGlyProPheAspLeuVall	Oy 621 ThrValLysHisGluGlyGlnIleLysTyrValAsı 	Qy 601 GlyIleLysValGluLysTyrIleAlaSerGlu	Qy 581 IleArgValLeuSerLeuPheAspGlyIleAlaTha	Qy 561 LeuGluGluPheGluProProLysLeuTyrPro	Qy 541 LeuArgArgArgLysAspTrpAsnMetArgLeu	Qy 521 AlaLysLeuGlnGluProTrpSerCysTyrMet	Oy 501 CysArgCysPheCysValGluCysLeuGluVal	Qy 481 SerTyrCysThrValCysCysGluGlyArgGluLeuLeuCys	Qy 461 GlnSerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAspGl	Oy 441 LeuSerCysGlyLysLysAsnProValSerPhet	Qy 421 SerArgGluArgMetAlaSerGluValThrAsn	Qy 401 ProProLysArgLeuLysThrAsnSerTyrGly
OValMetAlaSerLysAsnAspLysLeu 760	leLysValSerAlaAlaHisArgAlaArgTyr 740 	mAspLysLysAspIleSerArgPheLeu 720 NGACAAGAAAGACATCTCAAGATTCCTG 2511	ysGluGlyAspAsnArgProPhePheTrp 700 	rGluGlyThrGlyArgLeuPhePheGlu 680 		AsnAspValArgLysIleThrLysLys 640 	AlaserGluValCysAlaGluSerIleAlaValGly 620 	aThrGlyTyrLeuValLeuLysGluLeu 600 	ProAlaIleProAlaAlaLysArgArgPro 580 	rpAsnMetArgLeuGlnAspPhePheThrThrAspProAsp 560 	tCysLeuProGlnArgCysHisGlyVal 540 	LeuGluValLeuValGlyAlaGlyThrAlaGluAep 520 	uLeuLeuLeuCysSerAsnThrSerCys 500 	eTyrMetTyrAspGluAspGlyTyrGln 480 	1SerPheHisProLeuPheGluGlyGlyLeuCys 460 	laSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCys 440 	TyrGlyGlyLysAspArgGlyGluAspGluGlu 420

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SEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
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DSAASES PPPKRLKTNS YGGKDRGEDEESRERMAS EVTNNKGNLEDRCLSCGKKNPVS
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LEVLVGAGTAEDAKLQEPWSCYMCLPQRCHGVLRRRRXDWNMRLQDFFTTDPDLEEFEP
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 4006)

Chen, T., Ueda, Y. and Li, E.

Chen, T., Ueda, Y. and Li, E.

Domtias encoded by transcripts from an intronic promoter of Dnmtlas is expressed abundantly in ES cells and germ cells
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2572 TTCTGGGGTAACCTACCCGGAATGAACAGGCCCGTGATGGCTTCAAAGAATGATAAGCTC 2631
                                                                                                                    ThrThrLysSerAsnSerIleArgGlnGlyLysAsnGlnLeuPheProValValMetAsn 800
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                                                                                                                                                                                                                                                                                                                                                                                                                     TyrThrAspValSerAsnMetGlyArgGlyAlaArgGlnLysLeuLeuGlyArgSerTrp 840
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Direct Submission
Submitted (08-FEB-2002) Cardiovascular Research Center,
Massachusetts General Hospital, 149 13th Street, Charlestown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="de novo methylation"
/note="contains PHD and PWWP domains; alternatively
                                                          GluLeuGlnAspCysLeuGluPheSerArgThrAlaLysLeuLysLysValGlnThrIle
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/organism="Mus musculus"
/strain="12984/SvJae"
/db_xref="taxon:10090"
/chromosome="2"
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/gene="Dnmt3b6"
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/gene="Dnmt3b6"
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                                                         Submitted (17-MAY-1999) Department of Biology, Institution of Basic Medical Medical Sciences, Dong Dan San Tiao 5,
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Cloning of full-length Dnmt3b
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Yin, B., Chen, Y.T., Zhu, M.,
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| GluTrpAlaHisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnLysLys
AspGlyAspGlnGluGlyMetAspThrThrGlnValAspAlaGluSerArgAspGlyAsp
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/dev_stage="8-9 day old embryo"
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                     41
                                                                              21 IleIleValAsnGlyAsnPheSerAspGlnSerSerAspThrLysAspAlaProSerPro
                                                                                                                                                   1 MetLysGlyAspSerArgHisLeuAsnGluGluGluGlyAlaSerGlyTyrGluGluCys
ProValLeuGluAlaIleCysThrGluProValCysThrProGluThrArgGlyArgArg
                                                         ATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCCCTCACCC
                                                                                                                                ATGAAGGGAGACAGCAGCATCTGAATGAAGAAGAGGGGTGCCCAGCGGGTATGAGGAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-MAY-1999) Department of Biochemistry and Mole Biology, Institution of Basic Medical Sciences, Chinese Acamedical Sciences, Dong Dan San Tiao 5, Beijing City 100005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 4149)
Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and Shen,Y.
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Yin, B., Chen, Y.T., Z
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SEISADKLVALGLEFSCHFNLLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
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EGQIKYVNDVRRITKKNIELFPGFDVJGSPCNDLSNVNPARKGLYEGTGRLFFEFY
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AICTEEVCTPETRGRSSPANTERHSUTTSSLERORASPRITRGRGCRHHVQEVPUEPPTR
SRRRRASSSASTPWSSPASVDFMEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="methylates cytosine
/note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAF74518.1"
/db_xref="GI:8347126"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="Dnmt3b"
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532	ccastcttggaggcaatctgcacagagccagtctgcacaccagagaccagagggcgcagg 591
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	Prolygleuthrarggluthrlygaspthrargthrargsergluserproalavalarg 120
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	AspPheMetGluGluValThrProLysSerValSerThrProSerValAspLeuSerGln 200
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H 0	LysGlyPheSerTrpTrpProAlaMetValValSerTrpLysAlaThrSerLysArgGln 260
п о	28
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7 7	LysteuvalSerTyrarglysAlametTyrHisThrLeuGlulysAlaArgYalargAla 320
7 7	1 34 3 14
7 7	GlutrpalahisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnLysLys 360
7 7	е н
e 0	argargGluasniysSerargArgArgThrThrasnaspSerAlaAlaSerGluSerPro 400
- 0	ProProLysargLeuLysThrasnSerTyrGlyGlyLysaspargGlyGluAspGluGlu 420

<u>ن</u> و	421 SerAr 1672 AGCCG	421 SerargGluhrgMerAlaSerGluvalThrhanAsnLyBGlyAsnLeuGluhapArgCys 440
ò	441 LeuSe	rcysGlyLysLysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCys 460
qq	1732 TIGIC	CTGTGGAAAGAAGCCTGTGTTTTTTTTTTTTTTTTTTTT
ò	461 GlnSe	rCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAspGlyTyrGln 480
업	1792 CAGAG	TTGCCGGGATCGCTTCCTAGAGCTCTTCTACATGTATGATGAGGACGGCTATCAG 1851
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q	1912 TGCAG	ATGCTTCTGTGTGGAGTGTCTGGAGGTGCTGGTGGGCGCAGGCACAGCTGAGGAT 1971
ò	521 AlaLy	BERNATION BERN
Пр	1972 GCCAA	GCTGCAGGAACCCTGGAGCTGCTATATGTGCCTCCCTCAGCGCTGCCATGGGGTC 2031
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q	2658	2658

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                      Charlestown, MA 02129, USA
Sequence update by submitter
On Nov 18, 1999 this sequence
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-NOV-1999) CVRC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 3946)
Okano, M., Chijiwa, T., Sasaki, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okano, M.,
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Mus musculus DNA cytosine-5 methyltransferase
alternatively spliced, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charlestown, MA 02129, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xie,S., Okano,M. a
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning and characterization of a family (cytosine-5) methyltransferases Nat. Genet. 19 (3), 219-220 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okano, M. and Li
             /translation="MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
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/product="DNA cytosine-5
/protein_id="AAC40180.2"
/db_xref="GI:6449474"
                                                                                                                                          /function="de novo DNA methylation"
/note="alternatively spliced product;
                                                                                                                                                                                                                                                                             1. .3946
                                                                                                                                                                                                                                                                                                          /map="84.0 cM"
1. .3946
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Eutheria;
                                                                                                                                                                           gene="Dnmt3b"
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                                                                                                                                                                                                                                                                                       /gene="Dnmt3b"
                                                                                                                                                                                                                                                                                                                                          chromosome="2"
                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"/
                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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GDSTEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKROAMPGMEWVQWFGDGKF
SEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
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CYMCLPQRCHGVLRRKDWNNRLQDFFTTDPDLEEFEPPKLYBAIPAAKRRFIRVLSL
FDGIATGYLVLKELGIKVEKYIASEVCAESIAVGTVCHEGGIKYVNDVRKITKKNIEE
WGPFDLVIGGSPCNULSNNVPARKGLYEGTGRAFFEFFYHLMYTRFKEGDNRFFFMF
ENVVAMKVNDKKDISRFLACNPVMIDAIKVSAAHRARYFWGNLPGMNRIFGFPAHYTD
VSNWGRGARQKLLGSSWSVPVIRHLEAPLKDYFACE"

Percent Similarity:
Best Local Similarity:
Query Match: á а á S 밁 5 뭐 S 밁 S 밁 á 밁 Ś 밁 Ş 뮹 Ş 뮹 Ś 밁 S 망 Ś 밁 US-09-720-086-6 (1-859) x AF068628 Score: Alignment ORIGIN BASE COUNT ö : 749 689 141 629 121 569 101 509 449 389 329 269 201 181 161 8 61 41 21 \vdash LysG1yPheSerTrpTrpProAlaMetValValSerTrpLysAlaThrSerLysArgGln SerThrGluTyrGlnAspAspLysGluPheGlyI1eGlyAspLeuValTrpGlyLysI1e AspGlyAspGlnGluGlyMetAspThrThrGlnValAspAlaGluSerArgAspGlyAsp AspPheMetGluGluValThrProLysSerValSerThrProSerValAspLeuSerGln SerArgArgArgArgAlaSerSerSerAlaSerThrProTrpSerSerProAlaSerVal ArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaThrArg ProLysLeuThrArgGluThrLysAspThrArgThrArgSerGluSerProAlaValArg ThrGlyAspGlyAspArgAspAspGluValAspAspGlyAsnGlySerAspIleLeuMet SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAspMet ProValLeuGluAlaIleCysThrGluProValCysThrProGluThrArgGlyArgArg ATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCCCTCACCC IleIleValAsnGlyAsnPheSerAspGlnSerSerAspThrLysAspAlaProSerPro ATGAAGGGAGACAGCAGCATCTGAATGAAGAAGAGGGTGCCAGCGGGTATGAGGAGTGC MetLysGlyAspSerArgHisLeuAsnGluGluGluGlyAlaSerGlyTyrGluGluCys GATGGAGATCAGGAGGGTATGGATACCACAGAGGTGGATGCAGAGAGCAGAGATGGAGAC GACTTCATGGAAGAAGTGACACCTAAGAGCGTCAGTACCCCCATCAGTTGACTTGAGCCAG ThrArgHisSerAsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThr CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACCAGAGACCAGAGGCCGCAGG AGCACAGAGTATCAGGATGATAAAGAGTTTGGAATAGGTGACCTCGTGTGGGGGAAAGATC TCTCGGAGACGTCGAGCATCGTCTTCAGCAAGCACGCCATGGTCATCCCCTGCCAGCGTC CGAGGTCGGCAGGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCGGCTACCAGG ACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCCAAAGAGCCTCCCCCAGAATCACC ACAGGAGATGGAGACAGATGATGAAGTAGATGGGAATGGCTCTGATATTCTAATG TCAAGCTCCCGGCTGTCTAAGAGGGAAGGTCTCCAGCCTTCTGAATTACACGCAGGACATG 3.7e-222 4105.50 90.34% 90.34% 89.44% a (1-3946) ß Conservative: Mismatches: Indels: Length: Matches: Gaps: 3946 776 0 0 83 2 140 100 988 240 928 898 200 808 180 748 160 883 628 568 508 08 448 60 388 326

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දු පු	281	AlaksplysleuvalalaleudlyleuPheSerGlnHisPheAsnLeuAlaThrPheAsn 300 	
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a 8	1289	GAGTGGGCCCACGGTGGCTTCAAGCCTACTGGGATCGAGGGCCTCAAACCCAACAAGAG 1348 GTHBFOVATVATAAHLY8SeFIYASVATATGARGSEFARGSGFARGARHIEUGTUBFCAAT 380	
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ò	6 6	eAlaValGly 62	
셤	2009	aaagtacattgcctccgaagtctgtgcagagtccat	

3974 bp. mRNA linear ROD 08-JUN-2000 MLMs musculus DNA cytosine-specific methyltransferase isoform 8 (Dnmt3b) mRNA, complete cds. Mus musculus.
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 3974)
Yin, E., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and isoforms in mouse embryonic tissue Unpublished
2 (bases 1 to 3974)
Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and 2129 AATATTGAAGAGTGGGGCCCGTTCGACTTGGTGATTGGTGGAAGCCCATGCAATGATGTCTC 2188 2249 ITTTACCACTTGCTGAATTATACCCGCCCCAAGGAGGCGACAACCGTCCATCTTCTGG 2308 2369 GCATGTAACCCAGTGATGATGGATGCCATCAAGGTGTCTGCTGCTCACAGGGCCCGGTAC 2428 2455 2456 -----AGGATCTTCGCTTCCCTGCTCAC 2479 Shen, Y. Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue 2309 ATGTTCGAGAATGTTGTGGCCATGAAAGTGACAAGAAAAGACATCTCAAGATTCCTG 2368 741 PheTrpGlyAsnLeuProGlyMetAsnArgProValMetAlaSerLysAsnAspLysLeu 760 761 GluLeuGlnAspCysLeuGluPheSerArgThrAlaLysLeuLysLysValGlnThrIle 780 781 ThrThrLysSerAsnSerIleArgGlnGlyLysAsnGlnLeuPheProValValMetAsn 800 801 GlyLysAspAspValLeuTrpCysThrGluLeuGluArgIlePheGlyPheProAlaHis 820 2540 AGTGTACCGGTCATCAGACACCTGTTTGCCCCCTTGAAGGACTACTTTGCCTGTGAA 2596 841 SerValProValIleArgHisLeuPheAlaProLeuLysAspTyrPheAlaCysGlu 859 641 ABnIleGluGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAsnAspLeu 681 PheTyrHisLeuLeuAsnTyrThrArgProLysGluGlyAspAsnArgProPhePheTrp 701 MetPheGluAsnValValAlaMetLysValAsnAspLysLysAspIleSerArgPheLeu 721 AlaCysAsnProValMetIleAspAlaIleLysValSerAlaAlaHisArgAlaArgTyr AF151976.1 GI:8347136 LOCUS DEFINITION ORGANISM RESULT 11 AF151976 REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS SOURCE TITLE ВÞ g ò d d g q ò g 6 B 6 ò ò ò ò ò

Direct Submission Submitter(17-MAY-1999) Department of Biochemistry and Molecular Biology, Institution of Basic Medical Sciences, Chinese Academy of

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ACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCCAAAGAGCCTCCCCCAGAATCACC
                  ThrArgHisSerAsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThr
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KDRGBDEESRERMASEVTNNKGNLEDRCLSCGKKNPVSFHPLFEGGLCQGCRBRELE
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FDGIARGYLVLKELGIKVEKYLASEVCARSIAVGTYKHBGQIKVNUDURKITKKNIES
WGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFYHLLNYTRPKEGDNRPFFWMF
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                                                                                              GlnSerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAspGlyTyrGln
                                                                                                                                                            LeuSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCys
                                                                                                                                                                                                                                                                                         ProProLysArgLeuLysThrAsnSerTyrGlyGlyLysAspArgGlyGluAspGluGlu
                                                                                                                                                                                                                                                                                                                                      ArgArgGluAsnLysSerArgArgArgThrThrAsnAspSerAlaAlaSerGluSerPro
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                                   SerTyrCysThrValCysCysGluGlyArgGluLeuLeuLeuCysSerAsnThrSerCys
                                                                                                                                                                                                                            SerArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCys
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                                                                                                                                                                                                             AGCCGAGAACGGATGGCTTCTGAAGTCACCAACAACAAGGGCAATCTGGAAGACCGCTGT
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1676 500 420 1496 440 1556 1616 480 1436

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1856
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                                                      521 AlaLysLeuGlnGluProTrpSerCysTyrMetCysLeuProGlnArgCysHisGlyVal 540
                                                                                                                                                                    LeuGluGluPheGluProProLysLeuTyrProAlaIleProAlaAlaLysArgArgPro 580
                                                                                                                                                                                                                                                                                                                                     ThrvalLysHisGluGlyGlnIleLysTyrValAsnAspValArgLysIleThrLysLys 640
                                                                                                                                                                                                                                                                                                                                                                                          641 AsnileGluGluTrpGlyProPheAspLeuVallleGlyGlySerProCysAsnAspLeu 660
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                                                                                                           LeuargarglysaspTrpAsnMetArgleuGlnaspPhePheThrThrAspProAsp
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4089 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 3 (Dnutal) mRNA, complete cds.
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/translation="MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Baaic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product = "DNA cytosine-specific methyltransferase isoform
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia! Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 4089) Yin, E., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                               2 (bases 1 to 4089)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and Shen, Y.
                                                                                                                                                                                                               Cloning of full-length Dnmt3b cDNA and its alternative splicing Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="methylates cytosine in DNA"
/note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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/db_xref="taxon:10090"
/dev_stage="8-9 day old embryo"
1. .4089
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'organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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|gene="Dnmt3b"
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                                                                                    AF151971.1 GI:8347122
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ORGANISM
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AUTHORS
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81 ArgA	61 GlnProValValAsnLysSerLysValArgArgSerAspSerArgAsnLeuGluProArg 3	41 GluTrpAlaHisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnLysLys 3 	321 GlyLysThrPheSerSerSerProGlyGluSerLeuGluAspGlnLeuLysProMetLeu 340 	ValSerTyrArgLysAlametTyrHisThrLe 	sPheAsnLe CTTTAATCT	261 AlaMetProGlyMetArgTrpValGlnTrpPheGlyAspGlyLysPheSerGluIleSer 280	241 Ly8GlyPheSerTrpTrpDroAlaMetValValSerTrpLy8AlaThrSerLy8ArgGln 260	221 SerThrGluTyrGlnAspAspLysGluPheGlyIleGlyAspLeuValTrpGlyLysTle 240 	201 AspGlyAspGlnGluGlyMetAspThrThrGlnValAspAlaGluGerArgAspGlyAsp 220 	181 AspPheMetGluGluValThrProLysSerValSerThrProSerValAspLeuSerGln 200 	161 SerArgArgArgAlaSerSerSerAlaSerThrProTrpSerSerProAlaSerVal 180	141 ArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaThrArg 160	121 ThrargHisSerAsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThr 140 	101 ProLysLeuThrArgGluThrLysAspThrArgThrArgSerGluSerProAlaValArg 120	81 ThrGlyAspGlyAspArgAspAspGluValAspAspGlyAsnGlySerAspIleLeuMet 100 	61 SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAspMet 80		eValAsnGlyAsnPheSerAspGlnSerSerAspThrLysAspAlaProSerP
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741 PheTrpGlyAsnLeuProGlyMetAsnArgProValMetAlaSerLysAsnAspLysLeu 	721 AlaCysAsnProValMctIleAspAlaIleLysValSerAlaAlaHis	701 MetPheGluAsnValValAlaMetLysValAsnAspLysLysAspIleSerArgPheLeu 	681 PheTyrHisLeuLeuAsnTyrThrArgProLysGluGlyAspAsnArgProPhePh®Trp	61 32	41 72	12	52 GGTATTAAAGT	92		72	12	5 5 5	#15 Serryrcys1nrvalryscyschustyxtgstueneueucysserrasnnrsercys	, 10	1 2	1612 AGCCGAGAACGGATGGCTTCTGAAGTCACCAACAACAAGGGCAATCTGGAAGACCGCTGT 441 LeuSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCys	1552 CCACCCAAGCGCCTCAAGACAAATAGCTATGGCGGGAAGGACCGAG 421 SerArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnL	1498GAGAACAAAAGTCGAAGACGACAACCAATGACTCTGCTGCTTCTGAGTCCCCCC 401 ProProLysArgLeuLysThrAsnSerTyrGlyGlyJsAspArgGlyGluAspGluGlu

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VNDVRNITKKNIEEMGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFYHLLNYS
RPKEGDDRFPFWMFENVVAMKVGDKRDISRFLECNPVMIDAIKVSAAHRARYFWGNLP
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VLWCTELERIFGFPHYTDVSNKGRGARQKKLLGRSWSVPVIRHLFAPLKDYFACE"

1083 C 1096 g 925 L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 ACAGGCGATGGCGACGGG-----GAAGATGGGGGATGGCTCTGACACCCCCAGTC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 MetProLysLeuThrArgGluThrLysAspThrArgThrArgSerGluSerProAlaVal 119
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Matches:
Conservative:
Mismatches:
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LLVALGIEFSGHENLATPRILVSYRKAWTHALEKFKPRPAGKPFPSERGOEDEBDGLKPRNL
WAHGGFKPTGIEGLKPNNTQPVVNKSKVRRAGSRKLESRKYENKTRRTRADDSATSDV
CPAPKRLKTNCYNNGKDRGDEDGSREQMASDVANNKSSLEDGCLSCGRKNPVSFHPLF
EGGLGCTCRRFELELFWYNDDDGCYSCTVCCRGRELLLCSTSCCRCFCVECLEULV
GTGTTAAEAKLQEBNSCYNCLPGRSHULTARRUMNVRLQAFFTSDTGLSYEARLYDA
IPAARRRPIRVLSLPGGIATGYLVKELGIKVGKYVASEVCEBSIANGTVKHEGNIKY
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EIRGRRSSSRLSKREVSELLSYTGDGDEDDGGSDTPVMPALLRETRIRRSBSPA
VRTRNNSVSSRBRRRSPRSRGRQGRNHVDESPVERPATRSLERRATAAAGTPWPS
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Xie, S., Wang, Z., Okano, M., Nogami, M., Li, Y., He, W.W., Okumura, K. and Li, E.
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                                     761 GluLeuGlnAspCysLeuGluPheSerArgThrAlaLysLeuLysLysValGlnThrIle 780
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/product==10NA cytosine-5 methyltransferase 3 beta 1"
/protein_id="AAD53063.1"
/db_xref="GI:5823168".
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/organism="Homo sapiens"
/db xref="taxon:9606"
/chromosome="20"
/map="between D20S182 and D20S106; 39.9-50.2
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Xie, S. and Li, E.
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                                                                      MetArgLeuGlnAspPhePheThrThrAspProAspLeuGluGluPheGluProProLys
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Ni,J., Pradhan,S. and Robert
Direct Submission
Submitted (22-DEC-2000) New
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Ni,J., Pradhan,S. and Roberts,R.J.
Cloning, expression and characterization of human DNI unpublished
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                                                                                                                                                                                                         ArgGlyAlaArgGlnLysLeuLeuGlyArgSerTrpSerValProValIleArgHisLeu
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  SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAspMet
                                                                     ProValLeuGluAlaIleCysThrGluProValCysThrProGluThrArgGlyArgArg
                                                                                                                                                          IleIleValAsnGlyAsnPheSerAspGlnSerSerAspThrLysAspAlaProSerPro
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4267)
Xu,G.-L., Bestor,T.H., Bourc'his,D., Hsieh,C.-L., Tommerup,P. Bugge,M., Hulten,M., Qu,X., Russo,J.J. and Viegas-Pequignot, Chromosome instability and immunodeficiency syndrome caused mutations in DNA methyltransferase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-AUG-1999) Genetics a University, 701 West 168 St., New Location/Qualifiers
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2 (bases 1 to 4267)
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RATASAGTTMPSPPSSYLTIDLTDDYEDTHGTPPQSSSTPARLAQDSQQGGMESPQVE
ADSGDGSSEYODGKEFGIGDLVWGKIKGFSWMPAMVVSWKATSKRQAMSGMRWVQWF
GDGKKSEVSADKLVALGIFSQHFNLATTNKLVSYRKAMVHALEKARVRAGKTFPSSPG
GDSKESEVSADKLVALGIFSQHFNLATTNKLVSYRKAMVHALEKARVRAGKTFPSSPG
DSLEDQLKFMLEWAHGGFKPTGIEGLKPNNTQPENKTRRTADDSATSDYCPAFKELK
TNCYNNGKDRGDEDQSREQMASDVANNKSSLEDGCLSCGRKNPVSFHPLEGGLCQTC
RDRFLIELFYNYDDDGCYGSYCTVCCEGRELLLGSNTSCCRCFCVECLEULVGTTAAEA
KLQEFMSCYMCLPQRCHGVLRRRKDMNVRLQAFFTSDTGLEYEAFKLYPAIPARRRP
IRVLSLFDGJATGYLYLKELGIKVGKVVASEVCEESIAVGTVKHEGNIKVNNDVRNIT
KKNILEBWGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFYHLLINYKFNEDVEDR
PFFMMFENVVAMKVDJKRDISRFLECMPVMIDAIKVSAHRRARVFWGNLDGMNRFVIA
SKNDKLELQDCLEYNRIAKLKKVQTITTKSNSIKQGKNQLFPVVMNGKEDVLWCTELE
RIFGFPVHYDVSNWGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE"
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/product="DNA cytosine-5 methyltransferase 3B"
/protein_id="AAP04015.1"
/protein_id="AAP04015.1"
/db_xref="d1:6118092"
/translation="MEPSPEPPSLESMKGDTRHLNGEEDAGGREDSILVNGACSDQSS
/translation="MEPSPEPPSLESMKGDTRHLNGEEDAGGREDGGSDTPVMPKL
DSPPILEAIRTPEIRGRRSSSRLSKKEVSSLLSYTODLTGDDGGSDTDVMPKL
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3 6 1	231	GlylleGlyAspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetVal 25
g & 6	251	GGAATAGGGAALCICGIGIGGGGAAAGAT CAAGAGTICICGIGGGGGGGGGGGGGGGGGGGGGGGGGGG
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ò	371	ArgSerAspSerArgAsnLeuGluProArgArgArgGluAsnLysSerArgArgArgThr 390
С	1366	GAGAACAAGACTCGAAGACGACAAGACTCGAAGACGACACACAC
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Ор	-	3GGGATGAAGATCAGAGCCGAGAACAAATGGCTTCAGAT 1509
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đ	-	CTGGAAGATGGCTGTTTGTCTTGTGGCAGAAAAACCCC 1569
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ò	l	GluaspGlyTyrGlnSerTyrCyeThrValCysCyeGlu 488
qa	н	GACGATGGCTATCAGTCTTACTGCACTGTGTGCGAG 1689
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ò		ArgLeuPhePheGluPheTyrHisLeuLeuAsnTyrThr 688
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ò		1418ArgAlaArgTyrPheTrpGlyAsnLeuProGlyMet 748
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ò		rLysAsnAsplysLeuGluLeuGlnAspCysLeuGluPhe 768
οqα		aaagaatgataaactcgagctgcaggactgcttggaatac 2526
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cch co	2767	849	2707	829	2647	809	2587	789
SearCh completed: November 22, 2002, 10:52:58 Job time : 4989.5 secs	2767 TTCGCCCCTCTGAAGGACTACTTTGCATGTGAA 2799	PheAlaProLeuLysAspTyrPheAlaCysGlu 859	2707 CGTGGTGCCCGCCAGAAGCTGCTGGGAAGGTCCTGGAGCGTGCCTGTCATCCGACACCTC 2766	ArgGlyAlaArgGlnLy8LeuLeuGlyArgSerTrpSerValProValIleArgHisLeu 848	2647 ACTGAGCTCGAAAGGATCTTTGGCTTTCCTGTGCACTACACAGACGTGTCCAACATGGGC 2706	ThrGluLeuGluArgIlePheGlyPheProAlaHisTyrThrAspValSerAsnMetGly 828	2587 CAGGGGAAAAACCAACTTTTCCCTGTTGTCATGAATGGCAAAGAAGATGTTTTGTGGTGC 2646	789 GlnGlyLysAsnGlnLeuPheProValValMetAsnGlyLysAspAspValLeuTrpCys 808

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01-JUN-1995

Homo sapiens,

WO9514772-A1

cell typing; abnormal cell function;

Human gene signature HUMGS03426

14-AUG-1996 AAT21884;

(first

entry)

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;

11-NOV-1994;

93JP-0355504. 94WO-JP01916.

Matsubara K, (MATS/) MATSUBARA K. (OKUB/) OKUBO K. 12-NOV-1993;

WPI, 1995-206931/27. Okubo K;

Identifying gene signatures in for diagnosis of abnormal cell reflects relative abundance of tissues 3'-directed human cDNA library - function, by preparing cDNA that corresp. mRNA in specific human

e.g.

Claim 1; Page 991-992; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue The appearance frequency of a given GS ir determined (esp. using primers and probes probes derived from the from which it was derived CDNA S ğ

> SSSSS Sequence 301 BP; 96 A; 65 C; 63 G; sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. 66 T; 11 other

밁 á á 밁 S В á Вb á 밁 S Query Match Best Local Similarity Matches 241; Conserv 3690 3750 3630 3570 3510 3453 GATCAGATAGGAGCACAAACAGGAAGAGAATAGAGA----CCCTCGGAGGCAGAGTCTCCT 3509 240 180 121 61 ۲ AGTTTATATATATATGATAGATATGNG--NTATATATATAAAAAGGTACTGTTAACTACTG ACCACACAGGAAACCTTGAAGAAAACCAGTTTCTAGAAGCCGCTGTTACCTCTTGTTTAC 3689 CTCCCACCCCCGAGCAGTCTCAACAGCACCATTCCTGGTCATGCAAAACAGAACCCAAC 3569 TACA 3753 ACCACACAGGAAAACCTTGAAGAAAATCAGTTNCTAGGNNNNGCTGTTACCTCTTGTTTAC TAGCAGCAGGAGACGAGAACACCACACAAGACA-TTTTTCTACAGTATTTCAGGTGCCT TAGCAGCAGGGCGCTGAGAGAACACCACACACAGACACTTTCTACAGTATTTCAGGTGCCT 3629 CTNCCÁGCCACTGAGCTGNCGTGCCÁGCACCÁTTCCTGGTCÁCGCAAAAACAGAACCCATT 120 Conservative 4.2%; 0 Score 177.4; DB Pred. No. 3.9e-33 Mismatches DB 16; Length 57; Indels 301; 6 `` Gaps 297 179 239

\AT21884 ID AAT21884 standard;

CDNA to mRNA;

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Direct Submission
Submitted (03-JUN-1999) CVRC, Mass.
Charlestown, MA 02129, USA
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RESULT 2 AF331857 LOCUS DEFINITION

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AF331857

يأرا معاس

OLAND HAND BURNETH SHIP

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-MODEL=frame+_D2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool/US09720086/runat_18112002_092832_22195/app_query.fasta_1.4252
-Q=/cgn2 1/USPTO_spool/US09720086/runat_18112002_092832_22195/app_query.fasta_1.4252
-DB=GenEmb1 -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09720086 @GGN_1 111308 @runat_18112002_092832_22195 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-NABM_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
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Perfect score:
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DB seq length: 2000000000
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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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9: gb_pt:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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2054640 seqs, 14551402878 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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 175 ATCCTCGTCAACGGGCCTGCAGCGACCAGTCCTCCGACTCGCCCCCAATCCTGGAGGCT 234
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                                 SerSerLeuLeuSerTyrThrGlnAspLeuThrGlyAspGlyAspGlyGluAspGlyAsp
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Direct Submission
Submitted (03-JUN-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGKEEFIGDLWGKIKGFGWPPANVSWKATSKRQAMSGMRWQWFGDGKFSEVSADK
IVALGLESQHENLATENKLVSYRKAMYHALEKRKRARGAGKFPSSEPGDSLEDQLKPML
WAHGGFKPTGIEGLKPWTOPVVNKSKVRRAGSRKLESRKYENKTRRRTADDSATSD
CPAPRKIKTRYCYNNKORGDEODSREQMASDVANNKSSLEDGCLSGGRKMPVSEPHELE
EGGLCGTCRDRFLELFYMYDDGCYGSYCTVCCEGRELLLCSNTSCCRECVECUEULV
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IPAARRPTRVLELFDGTATGYLVLKELGIKVGKYVASEVVEESIRVGTYWHEGNIKY
VNDVRNITKKNIEEWGPFDLLVIGGSPCNDLESNVNPRAKGET
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GMNRPVLASKUDKLELODCLEYNRIAKLKKVOTITTKSNSIKQGKNQLPPVVNGKED
VLWCTELERIPGPPVYTDVSNNGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE"
1 1083 C 1096 g 925 L
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| prodeint id="AAD53063.1" |
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| pradeint id="MKGOTRHLNGEEDAGGREDSINSPWPAKLEREFRRERSESPA
VRTANNNSVSSREHREPSPRSTRGROGNUHUDESPVEFPATRSILGRATSAGTPWPS
PPSSYLITDLTDDTEDTHGTPQSSSTPYARLAQDSQQGGMESPQVEAD5GDDGDSSEYQ
       4F156488 4156488 4145 bp mRNA linear PRI 05-SEP-1999
Hömo sapiens DNA cytosine-5 methyltransferase 3 beta 1 (DNMT3B)
mRNA, complete cds.
                                                                                                                                                     Eukaryofe, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.

11 (bases 1 to 4145)
Xie,S., Wang,Z., Okano,M., Nogami,M., Li,Y., He,W.W., Okumura,K.
                                                                                                                                                                                                                                         expression and chromosome locations of the human DNMT3
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/map="between D20S182 and D20S106; 39.9-50.2
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gene="DNMT3B"
note="de novo DNA methyltransferase"
codon_start=1
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Matches:
Conservative:
Mismatches:
Indels:
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Gene 236 (1), 87-95 (1999)
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115. 2676
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Homo sapiens
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and Li, E.
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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                GlyMetAsnArgProVall1eAlaSerLysAsnAspLysLeuGluLeuGlnAspCysLeu
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                                                                                                                GCCATGAAGGTTGGCGACAAGAGGGACATCTCACGGTTCCTGGAGTGTAATCCAGTGATG
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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e: 4566.00 Matches: 853 ent Similarity: 100.00% Conservative: 0 Local Similarity: 100.00% Mismatches: 0 y Match: 9 Gaps: 0 9-720-086-8 (1-853) x AF331857 (1-4335)	1 MetLysglyaspThrargHisLeuAsnGlyGluGluAspAlaGlyGlyArgGluAspSer 20 	7 7	41 IleArgThrProGluIleArgGlyArgArgSerSerSerArgLeuSerLysArgGluVal 60 	61 SerSerLeuLeuSerTyrThrGlnAspLeuThrGlyAspGlyAspGlyGluAspGlyAsp 80 	81 GlyserAspThrProValMetProLysLeuPheArgGluThrArgThrArgSerGluSer 100 	101 ProalavalargThrargasnasnasservalserserargGluargHisargProser 120 	121 ProargSerThrargGlyArgGlnGlyArgABnHisValAspGluSerProValGluPhe 140 	141 ProalaThrargSerLeuargArgArgAlaThralaSerAlaGlyThrProTrpProSer 160 	161 ProProSerSerTyrLeuThrIleAspLeuThrAspAspThrGluAspThrHisGlyThr 180 	181 ProginSerSerSerThrProTyralaArgLeualaGinAspSerGinGinGiyGiyMet 200 	201 GluserProGlnValGluAlaAspSerGlyAspGlyAspSerSerGluTyrGlnAspGly 220 	221 LysGluPheGlynleGlyAspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpPro 240	241 AlametValValSerTrpLysAlaThrSerLysArgGlnAlametSerGlyMetArgTrp 260	261 ValGInTrpPheGlyAspGlyLysPheSerGluValSerAlaAspLysLeuValAlaLeu 280 	281 GlyLeuPheSerGlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLys 300 	301 AlaMetTyrHisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSerSer 320
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AF176228
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Submitted (06-AUG-1999) Genetics and Development,
University, 701 West 168 St., New York, NY 10032,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           Xu,G.-L., Bestor,T.H., Bourc'his,D., Hsieh,C.-L., Tommerup,N
Bugge,M., Hulten,M., Qu,X., Russo,J.J. and Viegas-Pequignot,
Chromosome instability and immunodeficiency syndrome caused
mutations in a DNA methyltransferase gene
Nature (1999) In press
                                                                                                                                                                                                                                                                                              Xu,G.L.
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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                                            /note="mutated in human chromosome immundeficiency disease known as IC alternative 5' exon 1B"
/codon_start=1
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                                                                                                                         'gene="DNMT3B"
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                                                                                                                                                                                      organism="Homo sapiens"
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                                                                                           gene="DNMT3B"
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requignot, E.
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                                                     RIFGFPVHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE"
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Alignment Scores:

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3897 bp mRNA linear PRI 05-SEP-1999 mRNA, complete cds.
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(Chases 1 to 3897)

Xie, S., Wang, Z., Okano, M., Nogami, M., Li, Y., He, W.W., Okumura, K. and Li, E.

Cloning, expression and chromosome locations of the human DNWT3 gene family Gene 236 (1), 87-95 (1999) TyrValAlaSerGluValCysGluGluSerIleAlaValGlyThrValLy8HisGluGly 620 2161 CCATTTGACTTGGTGATTGGCGGAAGCCCATGCAACGATCTCTCAAATGTGAATCCAGCC 2220 2461 GGGATGAACAGGCCCGTGATAGCATCAAAGATAAACTCGAGCTGCAGGTGCTTG 2520 2581 ATCAAACAGGGAAAAACCAACTTTTCCCTGTTGTCATGAATGGCAAAGAAGATGTTTTG 2640 2340 2341 GCCATGAAGGTTGGCGACAAGAGGGACATCTCACGGTTCCTGGAGTGTAATCCAGTGATG 2400 2521 GAATACAATAGGATAGCCAAGTTAAAGAAAGTACAGACAATAACCACCAAGTCGAACTCG 2580 2641 TGGTGCACTGAGCTCGAAAGATCTTTGGCTTTCCTGTGCACTACACAGAGGATCTCTAGC 2700 2701 ATGGGCCGTGGTGCCCGCCAGAAGCTGCTGGGAAGGTCCTGGAGCGTGCTGTCATCCGA 2760 640 260 9 680 761 GlutyrAsnArgileAlaLysLeuLysLysValGlnThrileThrThrLysSerAsnSer 780 700 720 TrpCysThrGluLeuGluArgllePheGlyPheProValHisTyrThrAspValSerAsn 820 IleLysGlnGlyLysAsnGlnLeuPheProValValMetAsnGlyLysGluAspValLeu 800 2281 TACTCACGCCCCAAGGAGGTGATGACCGGCCGTTCTTCTGGATGTTTGAGAATGTTGTA 741 GlyMetAsnArgProVallleAlaSerLysAsnAspLysLeuGluLeuGlnAspCysLeu 621 AsnIleLysTyrValAsnAspValArgAsnIleThrLysLysAsnIleGluGluTrpGly 641 ProPheAspLeuValIleGlyGlySerProCysAsnAspLeuSerAsnValAsnProAla ArglysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrHisLeuLeuAsn TyrSerArgProLysGluGlyAspAspArgProPhePheTrpMetPheGluAsnValVal 821 MetGlyArgGlyAlaArgGlnLyBLeuLeuGlyArgSerTrpSerValProValIleArg AlaMetLysValGlyAspLysArgAspIleSerArgPheLeuGluCysAsnProValMet HisLeuPheAlaProLeuLysAspTyrPheAlaCysGlu 853 AF156487.1 GI:5823165 RESULT 4 AF156487 LOCUS DEFINITION ORGANISM 2041 2761 1981 701 781 841 REFERENCE AUTHORS 601 661 681 801 ACCESSION VERSION KEYWORDS SOURCE JOURNAL QQ q q g ò 셤 ò 엄 ò qq S a ò g ò 임 ò g ò ò à ò g ð g

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10433969
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Xie,S. and Li,E.
Direct Submission
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KVGDKRDISRFLECNPVMIDAIKVSAAHRARYFWGNLPGMNRIFGFPVHYTDVSNMGR
GARQKLLGRSWSVPVIRHLFAPLKDYFACE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="DNA cytosine-5 methyltransferase 3 beta
/protein id="NAD53062.1"
/db_xref="GI:5823166"
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/map="20q11.2"
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|db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="de novo DNA methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="DNMT3B"
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AAAAACCCCGTGTCCTTCCACCCCTCTTTTGAGGGGGGGCTCTGTCAGACATGCCGGGAT 143 ArgPheLeuGluLeuPheTyrMetTyrAspAspAspGlyTyrGlnSerTyrCysThrVal 480	ysasnProValSerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysargAsp 46 	AlaSerAspValAlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArg 440	ThrasnCysTyrAsnAsnGlyLysAspArgGlyAspGluAspGlnSerArgGluGlnMet 420	ArgArgThrAlaAspAspSerAlaThrSerAspTyrCysProAlaProLysArgLeuLys 400	Lysvalnighighiauiyseinighysheudiuseinighyslyichuhshnyslninig 380	GCCCACTGGGATCGAGGGCCTCAAACCCAACAACACGCAACCA	LysProThrGlyIleGluGlyLeuLysProAsnAsnThrGlnProValValAsnLysSer 360	ProGlyAspSerLeuGluAspGlnLeuLysProMetLeuGluTrpAlaHisGlyGlyPhe 340	CATGTACCATGCTCTGGAGAAAGCTAGGGTGCGAGCTGGCAAGACCTTCCCCAGCAGC 10		GlyLeuPheSerGlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLys 300	ValGlnTrpPheGlyAspGlyLysPheSerGluValSerAlaAspLysLeuValAlaLeu 280 	GCCATGGTGGTGTCTTGGAAGGCCACCTCCAAGCGACAGGCTATGTCTGGCATGCGGTGG 894		AGGAGTTTGGAATAGGGGACCTCGTGTGGGGAAAGATCAAGGGCTTCTCCTGGTGGCCC 834	LvsGluPheGlvIleGlvAspLeuValTrpGlvLvsIleLvsGlvPheSerTrpTrpPro 240	GluserbroginValdluAlaAspSerGlyAspGlyAspSerSerGluTyrGlnAspGly 220	CCCCAGAGCAGCAGTACCCCCTACGCCCGAGCAGCAGGACAGCAGGAGGGGGGGCATG 714	ProGlnSerSerSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMet 200	CAGCTCTTACCATCGACCTCACAGACGACACAGAGGA	roProSerSerTyrLeuThrIleAspLeuThrAspAspThrGluAspThrHisG]	rgArgAlaThrAlaSerAlaGlyThrPro	CACGTTCCACCCGAGGCCGGCAGGGCCGCAACCATGTGGACGAGTCCCCCGTGGAC	

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Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.
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Xie, S., Okano, M. and Li, E.
Direct Submission
Submitted (28-MAY-1998) CVRC, Mass. Gen. Hospital, 149 13th Street, Charlestown, MA 02129, USA
3 (Dasse 1 to 4195)
Okano, M., Chilliwa, T., Sasaki, H. and Li, E.
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Submission
Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; 
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Accession Numbers AA116694, AA119979, AA17277, AA210568
AA407106, and AA575617"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'function="de novo DNA methylation"
          2386 CACCTCTTCGCCCCTCTGAAGGACTACTTTGCATGTGAA 2424
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/map="84.0 cM"
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/gene="Dnmt3b"
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/gene="Dnmt3b"
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/gene="Dnmt3b"
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TITLE
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1495 TGCTGCGAGGCCGAGAGCTGCTTTGCAGCAACACGAGCTGCTGCCGGTGTTTTCTGT 1554
                                                                                                                                                                                    1555 GTGGAGTGCCTGGAGGTGCTGGTGGGCACAGGGCACAGCGCCGAGGCTTCAGGAG 1614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGATGGCATCGCGACAGGCTACCTAGTCCTCAAAGAGTTGGGCATAAAGGTAGGAAAG 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1915 AATATCAAATACGTGAACGACGTGAGGAACATCACAAAGAAAAAAATATTGAAGAATGGGGC 1974
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                                                                                                                                  501 ValGluCysLeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGlu 520
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                                                                                                                                                       AlaSerGluValCysGluGluSerIleAlaValGlyThrValLysHisGluGlyAsnIle
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                                                          AAATATGTCAATGACGTCCGGAAAATCACCAAGAAAAATATTGAAGAGTGGGGCCCGTTC
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note="alternatively spliced"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
/dev_stage="8-9 day old embryo"
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 4223)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Mu, G.Y. and Shen, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 4223)
Yin, B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and
Shen,Y.
                                       2393 AAAGTGAATGACAAGACATCTCCAGATTCCTGGCATGTAACCCAGTGATGATCGAT 2452
                                                                                                                                                                      2573 AGTAGGACAGCAAAGTTAAAGAAGTGCAGAGACAATAACCACCAACGAACTCCATCAGA 2632
                                                                                                                                                                                                                                                                                                                   2693 ACTGAGCTCGAAAGGATCTTCGGCTTCCCTGCTCACTACACGGACGTGTCCAACATGGGC 2752
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    2213 GACTTGGTGATTGGTGGAAGCCCATGCAATGATCTCTCTAACGTCAATCCTGCCCGCAAA 2272
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                          663 GlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrHisLeuLeuAsnTyrSer 682
                                                                                                                         703 LysValGlyAspLysArgAspIleSerArgPheLeuGluCysAsnProValMetIleAsp 722
                                                                                                                                                                                                                                                                   763 AsnArgileAlaLysLevELysLysValGlnThrileThrThrLysSerAsnSerIleLys 782
                                                                                                                                                                                                                                                                                                                                                                  803 ThrGluLeuGluArgllePheGlyPheProValHisTyrThrAspValSerAnnMetGly 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2813 TTTGCCCCCTTGAAGGACTACTTTGCCTGTGAA 2845
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/organism="Mus musculus"
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503	84 GlyArgGluLeuLeuLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCys	Ş
483 1760	464 GluLeuPheTyrMetTyrAspAspAspGlyTyrGlnSerTyrCysThrValCysGysGlu 	음 성
463 1700	ysGlnThrCysArgAspArgPheLeu ::: TCAGAGTTGCCGGGATCGCTTCCTA	유 상
443 1640	4 ValAlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArgLy8AsnPro	D Qy
423 1580	4 TyrAsnAsnGlyLysAspArgGlyAspGluAspGlnSerArgGluGlnMetAlaSerAsp	B 6
403 1523	rCysProAlaProLysArgLeuLysThrAsnCys 	g gy
383 1466	gAlaGlySerArgLy8LeuGluSerArgLy8TyrGluAsnLy8ThrArgArgArgThr 	g 9
363 1406	GlyLeuLysProAsnAsnThrGlnProValValAsnLysSerLysValArg 	д Q
343 1346	24 SerLeuGluAspGlnLeuLysProMetLeuGluTrpAlaHisGlyGlyPheLysProThr 	B &
323 1286	AlaArgValArgAlaGlyLysThrPheProSerSerProGlyAsp CAGGGTTCGAGCTGGCAAGACCTTCTCCAGCAGTCCTGGAGAG	망 왕
303 1226	heAsnLysLeuValSerTyrArgLysAlaMetTyr 	용 성
283 1166	264 PheGlyAspGlyLysPheSerGluValSerAlaAspLysLeuValAlaLeuGlyLeuPhe	Db Qy
263 1106	alGlnTrp ACAGTGG	р Q
243 1046	GlyPheSerTrpTrpProAlaMetVal 	Db Qy
223 986	yrGlnAspGlyLysGluPhe aTCAGGATGATAAAGAGTTT	B &
203 926	erThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMetGluSerPro 	g 9
183 866	AspThrGluAspThrHisGlyFhrProGlnSer ::: GAAGTGACACCTAAGAGC	g &
163 833	4 ArgSerLeuArgArgArgAlaThrAlaSerAlaGlyThrProTrpProSerProProSer	Db Qq

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1462 GGGATCGAGGCCTCAAACCCAACAAGAAGCAACCAGTGGTTAATAAGTCGAAGGTGCGT 1521
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472 ATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACGAGGATGCTCCCTCACCC 531
                                                                                                                                                                          592 TCAAGCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACATG 651
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                                                                                                                                         51 SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyrThrGlnAspLeu 70
                                                                                                                                                                                                     71 ThrGlyAspGlyAspGly------GluAspGlyAspGlySerAspThrProVal 86
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="DNA cytosine-specific methyltransferase isoform
                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammaliai, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 4318)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                    (bases 1 to 4338)
(in,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and
                                                                                                                                                                                                       Cloning of full-length Dnmt3b cDNA and its alternative splicing
AF151969 4338 bp mRNA linear ROD 08-JUN-
us musculus DNA cytosine-specific methyltransferase isoform 1
(Dnmt3b) mRNA, complete cds.
AF151969
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/note="alternatively spliced"
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Conservative:
Mismatches:
Indels:
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Direct Submission
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Cloning and characterization of a
(cytosine-5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
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             /note="similar to EST sequences deposited in GenBank Accession Numbers AA116594, AA119979, AA177277, AA21 AA407106, and AA575617"
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/chromosome="2"
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SEISADKLVALGLFSQHFNLLATFNKLVSYRKAMYFTLEKARVRAGKTFSSSPGESLED
QLKPMLEWAHGGFKFTGIEGLKPNKKQPENKSRRTTNDSAASESPPKRLKTNSYGG
KDRGEDEESRERMASBYNNKGNLEDRCLSGGKKNPVSFHPLFEGGLCQSCKDRFFLEL
FYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVECLEVLVGAGTAEDAKLQEPWS
CYMCLPQRCHGVLRRRKDWNMRLQDFFTTDPDLEEFEPPKLVRAIPARAKRFFIRVLSL
FDGIATGSLVLKELGIKVEKYIASEVCAESIAVGTVAGEGDIKYVNDVRKITKNKIE
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EGGPDLVIGGSCKUNLSNVNPARKGLYEGTGRLFFEFYHLLNYTRPKEGDNRFPFWMF
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AICTEPVCTPETRGRRSSBRUSKREVSSLLNYTQDMTGDGDDDDDDDDGNGSDILMPK
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444 ValSerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysArgAspArgPheLeu 463 1880 1760 1820 1940 2000 2060 2180 2240 2421 GCCATCAAGGTGTCTGCTCACAGGGCCCGGTACTTCTGGGGTAACCTACCCGGAATG 2480 2061 GCTCCGAAGTCTGTGCAGAGTCCATCGCTGTGGGAACTGTTAAGCATGAAGGCCAGATC 2120 1407 ACCAATGACTCTGCTTCTGAG---TCCCCCCCACCAAGGCGCCTCAAGACAAATAGC 1463 503 602 543 562 622 742 523 642 662 682 1701 GGCCGTGAACTGCTGTGCAGTAACAACTGCTGCAGATGCTTCTGTGTGGAGTGT 404 TyrAsnAsnGlyLysAspArgGlyAspGluAspGluAspGluGlnMetAlaSerAsp 424 ValAlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArgLysAsnPro GlyArgGluLeuLeuLeuLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCys LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSer 1761 CTGGAGGTGCTGGTGGGCGCAGCCAGCTGAGATGCCAAGCTGCAGGAACCCTGGAGC 524 CystyrMetCysLeuProGlnArgCysHisGlyValLeuArgArgArgLysAspTrpAsn 1821 TGCTATATGTGCCTCCCTCAGCGCTGCCATGGGGTCCTCCGACGAGAAAGATTGGAAC 2001 GGAATTGCAACGGGGTACTTGGTGCTCCAAGGAGTTGGGTATTAAAGTGGAAAAGTACATT AlaSerGluValCysGluGluSerIleAlaValGlyThrValLysHisGluGlyAsnIle 2121 AAATATGTCAATGACGTCCGGAAAAATCACCAAGAAAATATTGAAGAGGGGGCCGTTC 643 AspLeuValileGlyGlySerProCysAsnAspLeuSerAsnValAsnProAlaArgLys GlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrHisLeuLeuAsnTyrSer 2241 GGTTTATATATGAGGGCACAGGAAGGCTCTTCTTCGAGTTTTACCACTTGCTGAATTATACC 544 ValArgLeuGlnAlaPhePheThrSerAspThrGlyLeu---GluTyrGluAlaProLys LeuTyrProAlaIleProAlaAlaArgArgArgProIleArgValLeuSerLeuPheAsp 583 GlylleAlaThrGlyTyrLeuValLeuLysGluLeuGlyIleLysValGlyLysTyrVal LysTyrValAsnAspValArgAsnIleThrLysLysAsnIleGluGluTrpGlyProPhe AlaileLysValSerAlaAlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGlyMet 683 ArgProLysGluGlyAspAspArgProPheTrpMetPheGluAsnValValAlaMet 504 603 623 723 484 563 663 g 음 g g G ò 8 8 8 8 ò ò ò 8 8 ठ व <u>ک</u> و ò 8 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-MAY-1999) Department of Biochemistry and Molecular Biology, Institution of Basic Medical Sciences, Chinese Academy Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 4278)
Yin,B., Chen,Y.T., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning of full-length Dnmt3b cDNA isoforms in mouse embryonic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-MAY-1999)
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Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus DNA cytosine-specific methyltransferase isoform
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                                                                  /translation="MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
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SRRRASSSASTPWSSPASVDEWEEVTEKSVSTPSVDLSQDGDQEGMDTTQVDAESIY
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                                                                                                                                                                                                                                                      note="alternatively
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CYMCLPQRCHGVLRRRKDMNMRLQDFFTTDPDLEEFEPPKLYPAIPAAKRRPIRVLSL
FDGIATGYLVLKELGIKVEKYIASEVCAESIANGTVEHEGQIKVUNDVRKITKKNIEE
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AHYTDVSNMGRGARQKLLGRSMSVFVIRHLFAPLKDYFACE"

1055 a 1113 c 1154 g 956 t

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Best Local Si Query Match: DB: Ş á S 밁 B S 밁 δ 밁 S 밁 S 밁 á 밁 Ś 당 Ş 망 В S 밁 밁 Š Score: Š 밁 S US-09-720-086-8 (1-853) Percent Similarity: Alignment 1042 No.: 889 652 592 532 472 412 244 184 144 829 769 104 709 164 124 87 71 51 36 21 $\boldsymbol{\mu}$ ValSerTrpLysAlaThrSerLysArgGlnAlaMetSerGlyMetArgTrpValGlnTrp GlyIleGlyAspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetVal GlnValGluAlaAspSerGlyAspGlyAspSerSerGluTyrGlnAspGlyLysGluPhe GTCAGTACCCCATCAGTTGACTTGAGCCAGGATGGAGATCAGGAGGGTATGGATACCACA SerSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMetGluSerPro MetProLysLeuPheArgGlu-----ThrArgThrArgSerGluSerProAlaVal ThrGlyAspGlyAspGly------GluAspGlyAspGlySerAspThrProVal SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyrThrGlnAspLeu ATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCCCTCACCC ATGAAGGGAGACAGCAGACATCTGAATGAAGAAGAGGGTGCCAGCGGGTATGAGGAGTGC Scores: SerTyrLeuThrIleAspLeuThrAspAspThrGluAspThrHisGlyThrProGlnSer AGGTCTCGGAGACGTCGAGCATCGTCTTCAGCAAGCACGCCATGGTCATCCCCTGCCAGC ArgSerLeuArgArgArgAlaThrAlaSerAlaGlyThrProTrpProSerProProSer ThrArgGlyArgGlnGlyArgAsnHisValAspGluSerProValGluPheProAlaThr ArgThrArgAsnAsnAsnSerValSerSerArgGluArgHisArgProSerProArgSer CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACAGAGACCAGAGGCCGCAGG ProIleLeuGluAlaIle------ArgThrProGluIleArgGlyArgArg GGAATAGGTGACCTCGTGTGGGGAAAGATCAAGGGCTTCTCCTGGTGGCCTGCCATGGTG CAGGTGGATGCAGAGAGCATATATGGAGACAGCACAGAGTATCAGGATGATAAAGAGTTT ACCCGAGGTCGGCAGGCCGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCGGCTACC CGAACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCCAAAGAGCCTCCCCCAGAATC ATGCCAAAGCTCACCCGTGAGACCAAGGACACCAGGACGCGCTCTGAAAGCCCCGGCTGTC ACAGGAGATGGAGACAGAGATGATGAAGTAGATGGGAATGGCTCTGATATT---CTA TCAAGCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACATG -----GTCGACTTCATGGAAGAAGTG----Similarity: 5.01e-186 3664.00 86.68% 80.60% 80.25% x AF151970 (1-4278)Length: Matches: Conservative: Gaps: Mismatches: Indels: 4278 702 53 66 50 SerPro . 103 1041 471 243 1101 163 888 143 828 123 708 8 651 70 591 50 531 35 263 223 203 981 183 948 768

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484 GlyargGluLeuLeuLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCys 503
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1162 GTGTCCTGGAAAGCCACCTCCAAGCGACAGGCCATGCCCGGAATGCGCTGGGTACAGTGG 1221
                                                                                                                                               HisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSerSerProGlyAsp 323
                                                                                                                                                                                                                                                                                                                                                                                   384 AlaAspAspSerAlaThrSerAspTyrCysProAlaProLysArgLeuLysThrAsnCys 403
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                           PheGlyAspGlyLysPheSerGluValSerAlaAspLysLeuValAlaLeuGlyLeuPhe 283
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Mus musculus DNA cytosine methyltransferase 3b6 (Dnmt3b6) mRNA, complete cds; alternatively spliced.
AY078427
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Chen, T., Ueda, Y. and Li, E.
Dnmtla2 encoded by transcripts from an intronic promoter of Dnmtla is expressed abundantly in Es cells and germ cells
Unpublished
2 (bases 1 to 4006)
2 (bases 1 to 4006)
2 (bases 1 to 4006)
Submitted (08-FBB-2002) Cardiovascular Research Center, Massachusetts General Hospital, 149 13th Street, Charlestown, MA 20129, USA
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                       2236 AATATGTCAATGACGTCCGGAAAATCACCAAGAAAATATTGAAGAGGGCCCGTTC 2295
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2416 CGCCCAAGAAGAGGACAAACGTCCATTCTTCTGGATGTTTCGAGAAAGTTTTGTGGCCATG
623 LysTyrValAsnAspValArgAsnIleThrLysLysAsnIleGluGluTrpGlyProPhe
                                                                                                      2296 GACTTGGTGGTGGAGCCCATGCAATGATCTCTCTAACGTCAATCCTGCCCGCAAA
                                                                                                                                                               663 GlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrHisLeuLeuAsnTyrSer
                                                                                                                                                                                     2356 GGTTTATATATGAGGCACAGGAAGGCTCTTCTTCGAGTTTTACCACTGCTGAATTATACC
                                                                                                                                                                                                                                                                                                                            703 LysValGlyAspLysArgAspIleSerArgPheLeuGluCysAsnProValMetIleAsp
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                                                                                 643 AspLeuValIleGlyGlySerProCygAsnAspLeuSerAsnValAsnProAlaArgLys
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DSAASESPPEKRLKTNSYGGKKRGEDEESRERMASEVTNNKGNLEDRCLSGGKKVEVS
FHPLFEGGLCOSCRNRETELFYMYDEDGYQSVCTVCCEGRELLLCSNTSCCRCFCVEC
LEVLVGAGTAEDAKLQEPWSCYMCLPGRCHGVLRRKKOMMRLLQFFTTDPDLEEEFEP
PKLYPAIPAKKRPIRVLSLFPGIATGYLLVLKELGIKVEKYIASEVCASSIAVGTVKH
EGQIKYVNDVRKITKKNIEWGPPDLVIGGSPCNDLSNNPARKGLYEGTGRLFFEFY
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/product="DNA cytosine methyltransferase
/protein_id="AAL85481.1"
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AF151975 4034 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 7
                                                                                                                                                                                                                                                                                                                          Direct Submission Submitted (17-MAY-1999) Department of Biochemistry and Molecular Biology, Institution of Basic Medical Sciences, Chinese Academy of Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005, P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="DNA cytosine-specific methyltransferase isoform
                                                                                                                                                                                                                               Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue upublished
2 (bases 1 to 4034)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                         Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 4034)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function="methylates cytosine in DNA"
/note="alternatively spliced"
/codon_start=1
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Mismatches:
Indels:
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/dev_stage="8-9 day old embryo"
1. .4034
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Matches:
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'db_xref="GI:8347135"
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gene="Dnmt3b"
                                                                                                 AF151975.1 GI:8347134
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81.40%
75.66%
74.56%
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Best Local Similarity:
Query Match:
DB:
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KEYWORDS
SOURCE
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                                                                                                      1853 TGCTATATGTGCCTCCCTCAGCGCTGCCATGGGGTCCTCCGACGCAAAAAATTGGAAC 1912
                                                                                                                                                              2093 GCCTCCGAAGTCTGTGCAGAGTCCATCGCTGTGGAAACTGTTAAGCATGAAGGCCAGATC 2152
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                             504 LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSer 523
                                                                                     543
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                                                                                                                                                                                                                                                                                                                                                                                                                                              643 AspLeuValileGlyGlySerProCysAsnAspLeuSerAsnValAsnProAlaArgLys 662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              783 GlnGlyLysAsnGlnLeuPheProValValMetAsnGlyLysGluAspValLeuTrpCys 802
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	344 GlyIleGluGlyLeuLysProAsnAsnThrGlnProValValAsnLysSerLysValArg 363
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Qy 7 Db 24	Qy 6 Db 23	Оу 6 Db 23	Qy 6 Db 22	Qy 6 Db 21	Qy 6 Db 21	Qу 5 Db 20	ОУ 5 Db 20	ь	Qy 5 Db 18	Qy 5	Qy 4 Db 17	Qy 4 Db 17	Qy 4 Db 16	Qy 4 Db 15	. Qy 4 Db 15	Qy 3 Db 14	Qy 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ThrargGlyArgGlnGlyArgAsnHisValAspGluSerProValGluPheProAlaThr 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 ArgSerLeuArgArgArgAlaThrAlaSerAlaGlyThrProTrpProSerProProSer 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 SerTyrLeuThrIleAspLeuThrAspAspThrGluAspThrHisGlyThrProGlnSer 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 ThrGlyAspGlyAspGly------GluAspGlyAspGlySerAspThrProVal
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Matches:
Conservative:
Mismatches:
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81.40%
75.66%
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Best Local Similarity:
Query Match:
DB:
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/db_xref="G1:8347126"
/translation="MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
AltTEPEVCTPETERGRRSSSRLEKREVSSLLAYTQDMTGDGDRDDEVDDGNGSDILMPK
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
P.R.China
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
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Mus musculus.

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae;

1 (bases 1 to 3946)

Okano, M., Xie, S. and Li, E.

Cloning and characterization of a family of novel man (cytosine-5) methyltransferases

Nat. Genet. 19 (3), 219-220 (1998)

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Anote="similar to EST sequences deposited in GenBank Accession Numbers AA116694, AA119979, AA177277, AA210568, 269. 2599
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Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327983.
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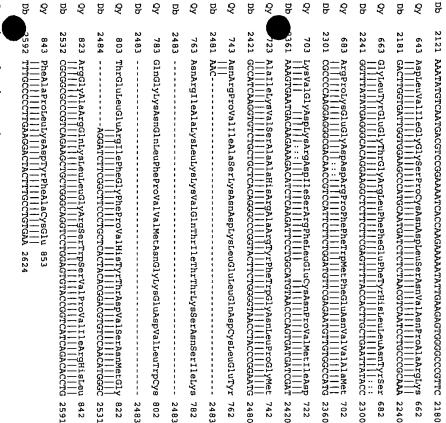
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                                                 AsnArgProValIleAlaSerLysAsnAspLysLeuGluLeuGlnAspCysLeuGluTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-MAY-1999) Department of Biochemistry and Molecular Biology, Institution of Basic Medical Sciences, Chinese Academy (Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning of full-length Dnmt3b cDNA isoforms in mouse embryonic tissue
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 3974)
Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C.
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Yin, B., Chen, Y.T., 2
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            GDSTEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
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76	res: arity milar	-8 (1	MetLysGly ATGAAGGG	IleLeuva] ::: ATTATCGT	Prolleter ::: CCAGTCTTC		ThrGlyAss ACAGGAGAT	MetProLye ATGCCAAAC	ArgThrare	Thrarggly acccgaggl	ArgSerber AGGTCTCGC	SerTyrLe			Glyllegly GGAATAGG	ValSerTri GTGTCCTGC	PheGlyAsp
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344 GlylleGluGlyLeulysBroAsnAsnThrGlnBroValValAsnLysSerLysValArg 363
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Search completed: November 22, 2002, 10:59:08 Job time : 4955.31 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3005)
Tale, S., Wang, Z., Okano, M., Nogami, M., Li, Y., He, W.W., Okumura, K. and Li, E.
                                                                                                                                Cloning, expression and chromosome locations of the human DNMT3 gene family Gene 236 (1), 87-95 (1999)
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Direct Submission
Submitted (12-MAY-1998) CVRC, Mass. General Hospital, 149 13th
Street, Charlestown, MA 02129, USA
3 (Dases I to 3005)
14 (Dases I to 3005)
Direct Submission
Direct Submission
Submitted (12-FEB-2001) CVRC, Mass. General Hospital, 149 13th
Street, Charlestown, MA 02129, USA
Sequence Update by submitter
On Feb 12, 2001 this sequence version replaced gi:4927369.
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                                                              81 AspSerGlyAlaSerGluLeuLeuProAsnGlyAspLeuGluLysArgSerGluProGln
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Eukaryota; Metazoa; Chordata; Craniata; Hominidae;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Ni.J., Pradhan,S. and Roberts,R.J.
Cloning, expression and characterization of human DN
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                                                                                                                                                                             SerArgLeuAlaArgGlnArgLeuLeuGlyArgSerTrpSerValProValIleArgHis 900
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                                                                                                                                                                                                                                                                                    LysGlnGlyLysAspGlnHisPheProValPheMetAsnGluLysGluAspIleLeuTrp 860
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AF068625.
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On Nov 18, 1999 this sequence
Location/Qualifiers
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Submitted (04-NOV-1999)
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Okano, M., Chijiwa, T., Sasaki, H.
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Xie,S., Okano,M. and Li,
Direct Submission
Submitted (28-MAY-1998)
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Cloning and characterization of a family
(cytosine=5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                      /translation="MPSGPGDTSSSSLEREDDRKEGEEOGENRGKEERQEPSATARK
VGRPGRKRKHPPVESSDTPKDPAVTTKSQPMAQDSGPSDLLPNGDLEKRSEPQEEGS
PAAGQKGGAPAEGEGTETPERSRAVENGCCYTKEGRGASAGEGKEGKQTNIESMKWE
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EPEYEDGRGFGIGELVWGKLRGFSWWPGRIVSWWMTGRSRAAEGTRWYMWFGDGKFSV
VCVEKLMPLSSFCSAFHQATYWQPMYRKAIVSVLQVASSRAGKLFPACHDSDESDSG
KAVEVQNKQMIEWALGGFQPSGPKGLEPPEEEKNPYKEVYTDMWVEPBAAAYAPPPA
KKPRKSTTEKFKVKBIIDERTRERLVYSVRQKCRNIEDIGISGSLNVTLHPLFIGG
MCQNKCKNCFILCAYQYDDGYQSYSTTCGGGREVLMCGNKNCCRFCVECVDLLVGPG
AAQAAIKEDPWNCYMCGHKGTYGLLRREDWPSRLQMFFANNHDQEFDPKVYPPVPA
EKRKPIRVLSLFDGJATGLLVLKDLGIQVDRYIASEVCDDSITVGMVTRQCKIMYVGD
VRSVTQKHIQEWGFPDLVIGGSFCNDLSIVRJKGVYGGTGRLFFEFYBLLHDARPK
EGDDRPFFWLFENVVAMGVSDKRDISRELSNFVMIDAKEVSAAHRARYFWGNLFGNN
RPLASTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKGKGOGJFPVFNMEKEDILW
RPLASTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKGKGOGJFPVFNMEKEDILW
RPLASTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKGKGOGJFPVFNMEKEDILW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to EST sequences deposited in Accession Numbers AA052791, AA111043, AA15489 AA756653, W58898, W59299, W91664, and W91665
                                                                                                                                                                                                       CTEMERVFGFPVHYTDVSNMSRLARQRLLGRSWSVPVIRHLFAPLKEYFACV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="DNA cytosine-5
/protein_id="AAC40177.2"
/db_xref="GI:6449468"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="contains"
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97.15%
96.27%
96.06%
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W91665"
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수 음 승	22 Aspai 271 GATCC	Asparglysaspolygluglugluglugluproargolylysolugluargolnolupro 41	d d
oy Ob	42 SerTh	SerThrThrAlaArgLysValGlyArgProGlyArgLysArgLysHisProProValGlu 61 	ර සි
<u>ک</u> ۾	62 SerG] 391 AGCAG		è a
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상 음	102 GluG] 511 GAGGA	GlugludiySerproAlaglyGlyGlyGlydlyAlaProAlagludlyGludlyAla 121 	S S
중 음	122 AlaG] 568 ACTGP	AlaGluThrLeuProGluAlaSerArgAlaValGluAanGlyCysCysThrProLysGlu 141	රි සි
<u>ن</u> و	142 GlyAr 628 GGCCC	GlyargGlyalaProAlaGlualaGlyLysGluGlnLysGluThrAsnIleGluSerMet 161 	ò a
ò 8	162 LysMe 688 AAAAT	LysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArg 181 	ò 8
송 원	182 Glnar 748 CAGCC	GlnargPrometProArgLeuThrPheGlnalaGlyAspProTyrTyrIleSerLysArg 201 	ò a
<u>ئ</u> م	202 LYBAI 808 AAACC	LysargaspGluTrpLeualaargTrpLysargGlualaGluLysLysAlaLysValIle 221 	ò q
à à	222 AlaGl 868 GCAGT	AlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSerGlnLysValGluGlu 241 	රු පි
<u>ک</u> ۾	242 Alase 928 GCCAG	AlaSerProProAlaValGinGinProThrAspProAlaSerProThrValAlaThrThr 261	රු පු
yo d	262 ProG1 988 CCTGA	ProGlubroValGlySerAspAlaGlyAspLy8AsnAlaThrLy8AlaGlyAspAspGlu 281 	8 6
oy Ob	282 ProGl	ProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuValTrpGlyLyELeuArg 301 	දු පු
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462 AlaGluLyeProLysValLyeGluIleIleAspGluArgThrArgGluArgLeuValTyr 481
11588 ACAGAGAACTAAAGTCAGAAATCATTGATGACGAAAAGGGGGTGGTGTT 1647 1708 GTCACCCTGGAGCACCCACTCTTGGAGGCATGTGCCAGAACTGTAAGAACTGCTTC 1767 1888 TGTGTGGATCTCTTGGTGGGGCCAGGAGCTGCTCAGGCAGTTAAGGAAGACCCCTGG 1947 2008 CCTTCTCGACTCCCAGATGTTCTTTGCCAATAACCATGACCAGGAATTTGACCCCCCCAAAG 2067 1228 GAGAAGCTCATGCCGCTGAGCTCCTTCTGCAGTGCATTCCACCAGGCCACCTACAACAAG 1287 1828 GGGGGCGTGAAGTGCTCATGTGTGGGAACAACAACTGCTGCAGGTGCTTTTTGTGTCGAG 1887 2068 GTTTACCCACCTGTGCCAGCTGAGAAGAAGCAGCCCATCCGCGTGCTGTCTCTTTGAT 2127 2128 GGGATTGCTACAGGGCTCCTGGTGCTGAAGGACCTGGGCATCCAAGTGGACCGCTACATT 2187 2188 GCCTCCGAGGTGTGTGTGGTCCATCACGGTGGGCATGGTGCGGCACCAGGGAAAGATC 2247 2248 ATGTACGTCGGGGGACGTCCGCAGCGTCACACAGAAGCATATCCAGGAGTGGGGCCCATTC 2307 2308 GACCTGGTGATTGGAGGCACTCCCTGCAATGACCTCTCCATTGTCAACCCTGCCCGCAAG 2367 1948 AACTGCTACATGTGCGGGCATAAGGGCACCTATGGGCTGCTGCGAAGACGGGGAAGACTGG 2007 401 461 521 561 581 601 602 ProSerArgLeuGlnMetPhePheAlaAsnAsnHisAspGlnGluPheAspProProLys 621 622 ValTyrProProValProAlaGluLysArgLysProlleArgValLeuSerLeuPheAsp 641 642 GlylleAlaThrGlyLeuLeuValLeuLysAspLeuGlylleGlnValAspArgTyrlle 661 662 AlaSerGluValCysGluAspSerIleThrValGlyMetValArgHisGlnGlyLysIle 681 682 MetTyrvalGlyAspValArgSerValThrGlnLysHisIleGlnGluTrpGlyProPhe 701 702 AspleuVallleGlyGlyGlySerProCysAsnAspLeuSerIleValAsnProAlaArgLys 721 382 LysLeuPheProValCysHisAspSerAspGluSerAspThrAlaLysAlaValGluVal 502 ValThrLeuGluHisProLeuPheValGlyGlyMetCysGlnAsnCysLysAsnCysPhe 542 GlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGlu 562 CysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrp 582 AsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrp 442 GluProGluAlaAlaAlaTyrAlaProProProProAlaLysLysProArgLysSerThr

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IMAGE:3492853, 1
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              cDNA Library Preparation: Life Technologies, Inc. (LLNL) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                    Direct Submission
Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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VGRPGRKRKHPPVESSDTPKDPAVTTKSQPMAQDSGPSDLLPNGDLEKRSERQEPSATARK
VGRPGRKRKHPPVESSDTPKDPAVTTKSQPMAQDSGPSDLLPNGDLEKRSERPQPEEGS
PAAGQKGGAPAEGEGTETPPEASRAVENGCCVTKEGRGASAGEGKEQKPTNIESMKME
GSRGRLRGGLGMESSLRQRPWERLTFQAGDPYYISKRKEDEMLARMKREAEKKAKVIA
VMNAVEENQASGESQKVEEASPPAVQQPTDPASPTVATTPEPVGGDAGDKNATKAADD
EPSTEMPLSSFCSAFHQATTWKQPMYRKAIYBVLQVASSRAGKLFPACHEDSDESDSG
KAVEVQNKQMIEWALGGFQPSGPKGLEPPEEEKNPYKEVYTDMWVEPEAAAYAPPPA
KKEPRKSTTEKPKVKEIIDERTRERLVYEVROKKGNNIEDLGISGGSLNVTLEHPLFIGG
MCQNCKNCFLECAYQYDDDGYQSYCTICGGGREVLMCGNNCCRCFCVECVDLLVGPG
AAQAAIKEDPWNCYMCGHKGTYGLLRREEDWPSRLQMFEANNHDDSFDPFKVYPVPA
EKKRIRVLSLFDGIATGLLVLKDLGIQVDRYIASVCGCRCFCVECVDLLVGPG
AAQAAIKEDPWNCYMCGHKGTYGLLTREEDWPSRLQMFEANNHDDSFDPFKVYPVPA
EKKRIRVLSLFDGIATGLLVLKDLGIQVDRYIASVCGCTGRLFFEFYRLLHDARPK
EGDDRPFFWLFENVVAMGVSUKKDISRDISRTLSNSVMIDAKEVSAAARRYFFMGLIAW
RPLASTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKGCKDQHFPVFMNEKEDILM
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/protein_id="AAH07466.1"
/db_xref="GI:13938621"
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/db_xref="taxon:10090"
/map="CZECH II"
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acagagaaacctaaggtcaaggagatcattgatgagggcgcacaagggagcgctggtgtat	ysglyse	rereega	ValThrLeuGluHisProLeuPheValGlyGlyMetCysGlnAsnCysLysBanCysPhe 	YsThr1]	GCACCAT	YsPheCy 	VEGINA	AGGAAG	882 ABNCYSTYFWELCYSG1YHisLySG1YThrTyrG1YLeuLeuArgArgArgArgG1UABDTrp 601	GACGGG	TTGACC	euSerLe	TGTCTCT	alAspAr	TGGACCG	lisGlnGl	ACCAGG	182 MetTyrvalGlyAspValArgServalThrGlnLy8HisIleGlnGluTrpGlyProPhe 701 	snProAl	ACCCTGO	GlyLeuTyrGluGlyThrGlyArgLeuBhePheGluPheTyrArgLeuLeuHi6AspAl	TCCTGCA	ArgProLysG1uG1yAspAspArgProPhePheTrpLeuPheG1uAsnVa1Va1AlaMet -	rovalme		AlaLysGluValSerAlaAlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGlyMe	ACCTTCC	AsnargProLeuAlaSerThrValAsnAspLysLeuGluLeuGluGluCysLeuGluHi	AGTGTCT	erAsnSe	5
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                  Submission
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Rodentia;
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16, *** SEQUENCING
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Direct Submission
Submitted (23-JUL-2002) Human Genome Sequencing
of Molecular and Human Genetics, Baylor College
navlor Plaza, Houston, TX 77030, USA
replaced (
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Baylor Plaza, Houston,
3 (bases 1 to 123936)
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are unknown.

This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: GWLV
Center clone name: CH230-282D16
Center clone name: CH230-282D16
Center clone name: CH230-282D16
Center clone vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of read Assembly program: Phrap; version 0.990329
Consensus quality: 9907 bases at least Q40
Consensus quality: 9923 bases at least Q30
Consensus quality: 101036 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
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Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                              Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Scie
University of Tokyo, Laboratory of Genome Structure Analysis, H
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
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Sugano, S., Suzuki, Y., Ol
Shibahara, T., Tanaka, T.
                                                                                                                                                                                                                                                                                                                                                                                                                    Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project
                                                                                                                                                                                                                      NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology, cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of
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Homo sapiens cDNA: FLJ21577 fis, clone COL06724, highly similar to
AF067972 Homo sapiens DNA cytosine methyltransferase 3 alpha
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/clone_lib="COL"
/note="cloning vector
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                                                                                                                                                                                                                                                                                                                                                                                                                ACACAGAAGCATATCCAGGAGTGGGGCCCATTCGATCTGGTGATTGGGGGGCAGTCCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrGlnLysHisIleGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGAAGCCCATCCGGGTGCTGTCTCTCTTTGATGGAATCGCTACAGGGCTCCTGGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgLysProIleArgValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTACGGGCTGCTGCGGCGAGAGGACTGGCCCTCCCGGCTCCAGATGTTCTTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCCCAGGCAGCCATTAAGGAAGACCCCCTGGAACTGCTACATGTGCGGGCACAAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACAACAACTGCTGCAGGTGCTTTTGCGTGGAGTGTGTGGACCTCTTGGTGGGGCCGGGG
TTCTTCTGGCTCTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCG
                                                                                                                                      TTCTTTGAGTTCTACCGCCTCCTGCATGATGCGCGCCCAAGGAGGAGGAGATGATCGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGGTGGGCATGGTGCGGCACCAGGGGAAGATCATGTACGTCGGGGACGTCCGCAGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGACTTGGGCATTCAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAACCACGACCAGGAATTTGACCCTCCAAAGGTTTACCCACCTGTCCCAGCTGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1-2191)
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610 361 590 301

421

241 550 181

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AF151974 4163 bp mRNA linear ROD 08-JUN-2000
Mus musculus DNA cytosine-specific methyltransferase 1soform 6
(Dnmt3) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
product="DNA cytosine-specific methyltransferase isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4163)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 4163)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
Shen, Y.
                                1082 AGGACCATTACTACGAGGTCAAAACTCCATAAAGGAGGGAAAGACCAGCATTTTCCTGTC 1141
                                                                                                                                                                                                                                                                                                                                                                                     Cloning of full-length Dnmt3b cDNA and its alternative splicing
                                                                                                                                                                                                                                                                               1142 TTCATGAATGAGAAGAAGACATCTTATGGTGCACTGAAATGGAAAGGGTATTGGTTTC 1201
                                                                                                                                                                                                                                                                                                                                                    1202 CCAGTCCACTATACTGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGC 1261
                                                                                                                                                                                                                                              851 PheMetAsnGluLysGluAspIleLeuTrpCysThrGluMetGluArgValPheGlyPhe 870
                                                                                                                                                                           831 ArgThr1leThrThrArgSerAsnSer1leLysGlnGlyLysAspGlnHisPheProval 850
                                                                                                                                                                                                                                                                                                                   871 ProValHisTyrThrAspValSerAsnMetSerArgLeuAlaArgGlnArgLeuLeuGly 890
902 CGATTTCTCGAGTCCAACCCTGTGATGATTGATGCCAAAGAAGTGTCAGCTGCACACAGG 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="methylates cytosine in DNA"
/note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/dev_stage="8-9 day old embryo"
1. .4163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in mouse embryonic tissue
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/db_xref="G1:8347131"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Dnmt3b"
297. 2816
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Mus musculus
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AUTHORS
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JOURNAL
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/ Lranslation="WKGDSRHLNEEGASGYEECIIVNGNFSDQSSDTKDAPSPPULE
ATCTEPCTPETRGRESSELSKEWSESLLAYTOPMTGODEDDEVDGGGGGSDILMPR
ATCTEPCTPETRGRESSELSKEWSESLLAYTOPMTGODEDDEVDGGGGGSDILMPR
ATCTEPCTPETRGRESPASTRISKEWSESLLAYTOPMTGODEDDEVDGGGGSDILMPR
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GDSTEYQDDERFGTGDLWGMSKIKGFSWMPAMVYSKTSKRGAMGGRAWVGWFGDGKF
SEISADKLVALGILSGOTENWGRKIKGFSWMPAMVYSKTSKRGATGKRGWFEDGKF
SEISADKLVALGILSGOTENWGRIKGPSWATTINDSAASESPPRKLKTNNSYGG
KORGEDESRERMAGEVTNKKAUSPRKCASCKEKDENELEL
FYNYDEDGYGCFGRELLICSNYTSKRCYCECLECTLYGAGTARDAKLOEPNS
CYMCLPQRCHGVLRRKDWNRALODFFTTDPDLEEFEPPKLYFRAIPARARPIRVLSI
FOGIATGYLVLKELGIKVFRYTASEVCASSIANGYTHREQUIKYNDVRRTITKKNIEE
WGPFDLYIGGSPCNDLSNYNPARKGIYEGTGRLFFFFYHLLNYTRPKGEDNRFFFWHF
ENVVAMKVNDKCJISRFALKTORFYTISSTGGGROUFFFFYHLNYTRPKGEDNRFFFWHF
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ELVDCLEFFSTARLKKVVOTITTKSNSTRGGROUFFFVHUNTGKDDVLWCTELERIFGFF
AHYTDVSUMGRGARGKLLGRSNSVFVTHLFRAPLKDYFACE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 CCAAGTAAACGTAGCGCAGCGATCGGCGCCGGAGATTCGCGAAACCCGACACTCCGCGCCG 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 -------LeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGlu 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 GluGlySerProAlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyAlaAla 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 TATGAGGAGTGCATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGAT 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 ArgGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArgGlnArgProMetPro 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ProSerThrThrAlaArgLysValGlyArgProGlyArgLysArgLysHisProProVal 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GluSerGlyAspThrProLys------AspProAlaValileSer 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 LysSerProSerMetAlaGlnAspSer------GlyAlaSerGlu 86
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Matches:
Conservative:
Mismatches:
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2228.50
61.30$
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196 TyrTyrIleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGlu 215

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574	555 CysArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAla	Ş
7	77 TCCTACTGCACCGTGTGCTGTGAGGGCCGTGAACTGCTGCTGTGCAGTAACACAAGCTG	B
554	erTyrCysThrIleCysCysGlyGlyArgGluValLeuMetCysGlyAsnAsnAs	Ş
534 1676	515 GlnAsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGln	유왕
514 1616	1557 TTGTCCTGTGGAAAGAAGAAGAACCCTGTGTCCTTCCACCCCCTCTTTGAGGGTGGGCTCTGT	B 8
· UI	97 AGCCGAGAACGGATGGCTTCTGAAGTCACCAACAACAACAAGAGCAATCTGGAAGACCGCTG	} }
494	75 ThrArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAsp	. Q
4.	46 CGCCTCAAGACAAATAGCTATGGCGGGAAGGACCGAGGGGAGGATGAGGA	Db
474	erThrAlaGluLysProLysValLysGluIleIleAspGl	Ş
4.	::: AACCAATGACTCTGCTGCTGTGAGTCCCCCCAACCCAA	ф
ال 4.	yrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaPro	δ°
4		문 :
ω A	16 ProSerGlyProLysGlyLeuGluProProGluGluGluLysAsnProTyrLysGl	Ş
1340	GCCCATGCTGGAGTGGGCCCACGGTGGCTTCA	дb
415	luValGlnAsnLysProMetIleGluTrpAlaLeuGlyGlyPhe	Ş
N	42 GCCAGGGTTCGAGCTGGCAAGACCTTCTCCAGCAGTCC	Db 2
ו ס	376 AlaSerSerArgAlaGlvIvsIenDheDroValCvsHisAsnSerAsnGluSerAsn	Ş
N .	82 CTGGCTACCTTCAATAAGCTGGTTTCTTATAGGAAGGCCATGTACCACACTCTGGAGAA	뭥
7	AsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGln	Š
μ	TCTGCTGACAAACTGGTGGCTCTGGGGCTGTTCAGCCAGC	В
355	eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPhe	γQ
\vdash	;;; ;;;	Db
335	laAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLy	Ş
1061	TGTGGGGAAAGATCAAGGGCTTCTCCTGGTGGCCTGCCATGGTGGTGTCCTGGA	문
315	γίγsLeuArgGlγPheSerTrpTrpProGlγArgIleValSerTr	δ
1001	GACAGCACAGAGTATCAGGATGATAAAGAGTTTGGAATAGGTGA	B
295	pGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluL	Ş
941	882 GTTGACTTGAGCCAGGATGGAGATCAGGAGGGTATGGATACCACACAGGTGGATGCAGAG	망
275	.laThrThrProGluProValGlySerAspAlaGlyAspLysAs	ş
881	834 GTCGACTTCATGGAAGAGTGACACCTAAGAGCGTCAGTACCCCATCA	망
255	lGluGluAlaSerProProAlaValGlnGlnProThrAsp	Ş
833	792GCATCGTCTTCAGCAAGCACGCCATGGTCATCCCCTGCCAGC	DЪ
235	216 LysLysAlaLysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGlu	Ş
791	768 GCTACCAGGTCTCGGAGACGTCGA	рb

RESULT 8 AC009474 LOCUS	Qy 894 Db 2757	Qy 87; Db 269;	Qy 854 Db 2637	Qy 834 Db 2577	Qy 814 Db 2517	Qy 794 Db 2457	Oy 774 Db 2397	Qy 754 Db 2337	Qy 734 Db 2277	Qy 714 Db 2217	Qy 694 Db 2157	Qy 674 Db 2097	Qy 654 Db 2037	Qy 634 Db 1977	Qy 615 Db 1917	Qy 595 Db 1857	Qy 575 Db 1797	Db 1737
AC009474	SerValProValIleArgH	TyrThrAspValSerAsnMetSe	GluLysGluAspIleLeu'	ThrThrArgSerAsnSerI	GluLeuGlnGluCys	PheTrpGlyAsnLeuProGly	GluSerAsnProValMetII GCATGTAACCCAGTGATGAT	LeuPheGluAsnValValA: :::	PheTyrArgLeuLeuHisAspAlaAr	SerIleValAsnProAlaA TCTAACGTCAATCCTGCCC	HislleGlnGluTrpGlyPro	MetValArgHisGlnGlyLysI)	GlyIleGlnValAspAr	lleArgValLeuSerLeuPhe	GlnGluPheAspProPi ::: 	LeuArgArgArgGluAspTrp CTCCGACGCAGGAAAGATTGG	AlaIleLysGluAspProT	TGCAGATGCTTCTGTGTGG
168651 þp	isLeuPheAlaProLeuLy ACCTGTTTGCCCCCTTGAA	cArgLeuAla	8-8	leLysGlnGlyLysAsp ::: CAGACAGGGCAAAAAC	LeuGluHisGlyArgIleAla CTGGAGTTCAGTAGGACAGCA	ProGlyMetAsnArgProLeuAlaSe 	leAspAlaLysGluValSerAlaAlaH CGATGCCATCAAGGTGTCTGCTC	laMetGlyValSerAsp ::: CCATGAAAGTGAATGAC	AlaArgProLysGluGlyAspA ACCCGCCCCAAGGAGGGCGACA	rglysGlyLeuTyrGluGlyThrGlyArgLeuPh GCAAAGGTTTATATGAGGGCACAGGAAGGCTCTT	coPheAspLeuValIle 	CAAATATGT	9TYrIleAlaSerGluVal :{ STACATTGCCTCCGAAGTC	rLeuPheAspGlyIleAlaThrGlyLeuLeuVa1 TCTGTTTGATGGAATTGCAACGGGGTACTTGGTG	COLYSVAlTyrProPro ::: CAAGTTGTACCCAGCA	TrpProSerArgLeuGlnMetF 	TPASNCYSTYrMetCys GGAGCTGCTATATGTGC	AGTGTCTGGAGGTGCTGGTGGGCGCAGGCAC
DNA lin	LysGluTyrPheA: ::: AAGGACTACTTTGG	AArgGlnArgLeuLeu :::: CGTCAGAAGCTGCTC	PheG:	spGlnHisPhePro :: ACCAGCTTTTCCC	lealaLysPheSerLysVa 	AlaserThrValAsnAsr ;;;; ATGGCTTCAAAGAATGAI		rAspLysArgAspIle 	ACC	GlyThrGlyArs ggCACAGGAAGO	[leGlyGlySerPro ATTGGTGGAAGCCC <i>H</i>	lGlyAspValArgSei 	erGluValCysGluAspSet CCGAAGTCTGTGCAGAGTCC	GlyLeuLeuVal 	COValProAlaGlu ::: CAATTCCTGCAGCO	heph 	tCysGlyHisLysGlyThrTy 	GTGGGCGCAGGC
near PRI 08	AlaCys 911 [GCCTGT 2810	JeuGlyArgSerTrp	lyPheProValHis CTTCCCTGCTCAC	ProValPheMetAsn	ValArgThrile ::: GTGCAGACAATA	.AsnAspLysLeu ;AATGATAAGCTC	isArgAlaArgTyr CAGGGCCCGGTAC	leSerArgPheLeu CTCAAGATTCCTG	ArgProPhePheTrp GTCCATTCTTCTGG	LeuPhePheGlu CTCTTCTTCGAG	roCysAsnAspLeu ATGCAATGATCTC	3SerValThrGlnLγs ::: ::: SAAAATCACCAAGAAA	erileThrValGly	1LeuLysAspLeu : : : CTCAAGGAGTTG	GluLysArgLysPro ::: GCCAAAAGGAGGCCC	eAlaAsnAsnHisAsp 	ThrTyrGlyLeu ::: ::: !TGCCATGGGGTC	Æ
-NOV-200		93	2696	2636	2576	1 813 2516	793	773	753	1 733	1 713	693	2096	2036	633	1916	1856	1796

linear PRI 08-NOV-2000

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VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
NEIGHBORING SEQUENCE do the left is RPI1-547F18; the clone sequenced to the right is RPI1-44B4, 200 base pair overlap. Actual end of this clone is at base position 18711 of RPI1-44B4.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="similar to EST Al123298 (NID:g3539064) ov48c08.xl"
6210. 16348
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25405 - 25822 - 25822 - 25811) wo95h11.x1"
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6209. 16345
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827, 4198
rpt_family="MER1_type"
656, 6129
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/rpt_family="L1"
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/rpt_family="MER2_
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                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (24-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 168651)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168651)
Sulston, J. B. and Materston, R.
Sulston, J. B. and Materston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
Homo sapiens BAC clone RP11-179G23 from 2, complete sequence.
AC009474
AC009474.4 GI:8748849
                                                                                                                                                                                                                                                                        2 (bases 1 to 168651)
Mulvane, E., Stoneking, T., LaPlant, Y. and McDill, B.
The sequence of Homo sapiens BAC clone RP11-179G23
                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 168651)
Waterston, R.H.
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ProThrAspProAlaSerProThrValAlaThrThrProGluProValGlySerAspAla
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                                             75971 AGTGAGGAAGAGTGCCAGAACATCAAGGACCTTTGTGTGTCTCTTGTGAGAGCCTCAATGT
                                                                                                          75913 AAAAAAGCTCGACATCAAGGAGATTGTTGATGAAC--ACAGAAGAGTAGTTAGTGTACAA
                                                                                                                                                                    75793 GGGAGGCTGAGGCAGGAGAATCACTTGAACCAGGGAGTCGGAGGTTACAGTGAGCCGAGA 75852
                                                                                                                                                                                                                                                                                              75733 CTACTAAAAAGTACCAAAATAGCTGGACATGGTGGCATGTGCCTGTAATCCCAGCTACTG
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                                                                                                                                                                                                                                                                 466
                                                             482 uValArgGlnLysCysArgAsnIleGluAspIleCysIleSerCysGlySerLeuAsnVa
502 lThrLeuGluHisProLeuPheValGlyGlyMetCysGlnAsnCysLysAsnCysPheLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 TyrAlaProProProProAlaLysLysProArgLysSerThrAlaGluLys------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGlu
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                                                                                                                                                                                                                                                                                                                                                        ATCACGACGTCAGGAGATAGAGACCTGACATGGTCAGGCCAACATGGTGAAACCCCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeuSerSer
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76031 CACTCTGGAACAGCCCCTCTTCATGCTAGGAATATGACGACATTGCAAGAACTGCTTCCT 76090
                                                          76091 GGAATATGCATACCAGTATGATGAAGAAGGCTATCAGTTCTGCTGCACCATCTGCTGCTG 76150
                                                                                                             76151 TGGGCACCAGGTGCTCATGTGCTGG----AACAACTGCTGCTGCGGTGCTTTTGCGTGGAGTG 76207
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                            522 uGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrileCysCysGl 542
                                                                                        542 yGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGluCy 562
                                                                                                                                                sValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAs 582
                                                                                                                                                                                                              nCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrpPr 602
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AF068627 MENA 11near ROD 06-DEC-1999 MENA linear ROD 06-DEC-1999 Mus musculus DNA cytosine-5 methyltransferase 382 (Dnmt3b) mRNA, alternatively spliced, complete cds.
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GDSTEYODKEFGTGDLWAKIKGFSWPAMVSWRALTSKOADFGOWNYWRGDGKF
SELSADKLVALGLESQHFULFFUKLUS YRKAMYHTLEKKRYRAKTFSSFSDESLED
OLKPMLEWAHGGFKPTGIEGLKPNKKQPENKSRRRTTNDSAASESPPRKLKTNSYGG
KDRGEDESSRERMASEYTWKRANLENCLSCRKOPVSFRHETFEGGLGGSRDRFLEL
FYWYDEDGYGYCTVCCEGRELLLGSNTSCCRCFCVECLEVLVGAGTAEDAKLQEPWS
CYMCLPQRCHGVLRRRKDWMRLQDFFTTDPDLEEFEPPKLYPAIPAARRRPIRVLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street, Charlestown, MA 02129, USA. Sequence update by submitter on Nov 18, 1999 this sequence version replaced gi:3327981.
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AlcTEPVCTPFTRGTRSSRLSKRESSESSLLKPTQDMTGDGDDBVDDGVDGSDDLDAPK
LTRETKOTFTRSESPAVRTRHSNGTSSLERORASPRITTRGRQGRHHVQEYPVEPPATR
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Xie,S., Okano,M. and Li,E.
Direct Submission
Submittered (28-Mar-1998) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
3 (bases 1 to 4135)
Okano,M., Chijiwa,Tr., Sasaki,H. and Li,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 4135)

Ckano, M., Xie, S. and Li, E.
Cloning and characterization of a family of novel mammalian DNA (cytosine-5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
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Accession Numbers AA116694, AA119979, AA17727, AA210568,
AA407106, and AA575617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Damt3b"
/function="de novo DNA methylation"
/function="de novo DNA methylation"
/funct="allernatively spliced product; contains Cys-rich
region; C-terminal region is similar to corresponding
region of DNA cytosine-5 methyltransferase 3A"
/codon start=1
/product="DNA cytosine-5 methyltransferase 3B2"
/procedin_id="AAC40179-2"
/fub_xref="dis449472"
                             77138 CCATTGGGCAAGGCAAAGACTGTTGCGTGAGTCATGGAGCATAGCAGTCACTTGCCAATT 77197
881 rArgLeuAlaArgGlnArgLeuLeuGlyArgSerTrpSerValProVallleArgHisLe 901
                                                                                                                                 77198 CTTCCCTCCACTGAAGGGGTATTTTGCTTGTGTG 77231
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                                                                                                           901 uPheAlaProLeuLysGluTyrPheAlaCysVal
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chromosome="2"
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ςυ, FDGIATGYLVLKELGI KVEKYI ASEVCAESI AVGTVKHEGQI KYVNDVRKI TKKNI EE WGFFDLVI GGS FCNDLSNVNPARKGLYEGTGRLFFE FYHLLLWYMRKEGKNR PFWMFE ENVVANKVNDKKDI SRFLACNPVMI DDA IKVSAJAIRAKYEMGNL PGWNFPWASKKNDL ELQDCLEFSRTAKLKKVQTITTKSNSI RQGKNQLFPVVNNGKDDVLMCTELER I FGFPAYTDVSNMGRGARQKLLGRSNSVPVL RHLFAFLKDYFACE" 1048 ი 1106 g

Percent Similarity:
Best Local Similarity:
Query Match:
DB: 5 문 В á 밁 S 밁 Ş 멂 5 밁 Ş В Ş Sn Score: S 밁 ð g δ ₽ á 밁 Ś 밁 Ś 밁 Ş BASE COUNT ORIGIN 밁 Alignment Scores: No . : 103 377 317 620 560 147 500 440 140 389 197 137 720-086-7 (1-912) x AF068627 196 680 187 167 123 84 79 73 56 LysHisPro---ProValGluSerGlyAspThrProLysAspProAlaVallle-----77 36 23 740 GCTACCAGGTCTCGGAGACGTCGA-16 AlaAlaGluArgGluGluAspArgLysAspGlyGluGluGluGluProArgGlyLys GluGlySerProAlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyAlaAla 122 CCAGACGCGGGATCTCCCCTCCCCCATCCATAGTGCCTTGGGACCAAATCCAGGGCCTTC 256 GCTGTCCGAACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCAAAGAGCCTCCCCC 679 ArgGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArgGlnArgProMetPro 186 ATTCTAATGCCAAAGCTCACCCGTGAGACCAAGGACACCAGGACGCGCTCTGAAAGCCCG 619 CAGGACATGACAGGAGATGGAGACAGAGATGATGAAGTAGATGATGGGAATGGCTCTGAT 559 GGCCGCAGGTCAAGCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACG 499 ------CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACCAGAGACCAGA 439 GluThrLeuProGluAlaSerArgAlaValGluAsnGlyCysCysThrProLys-----GCTCCCTCACCC-----TATGAGGAGTGCATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGAT 376 AlaSerGlu---LeuLeuProAspGlyAspLeuGluLysArgSerGluProGlnProGlu 102 AlaGlnAsp-----CCTCACGACAGGCCCGCTGAGGCTTGTGCCAGACCTTGGAAACCTCAGGTATATACCTTT ${\tt GluGluArgGlnGluProSerThrThrAlaArgLysValGlyArgProGlyArgLysArg}$ ĠĊĠĠĊĊCAAGTAAACGTAGCGCAGCGATCGGCGCCGĠAĠATTCGCĠĀĀĊĊĊ-----GAC AlaGluAlaGlyLysGluGlnLysGluThrAsnIleGluSerMetLysMetGluGlySer 166 -----SerLysSerProSerMet TyrTyrlleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGlu 215 AGAATCACCCGAGGTCGGCAGGGCCGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCG 739 ArgLeuThr-----1043 1.62e-80 2226.00 59.71% 46.52% 45.11% (1-4135)Length:
Matches:
Conservative:
Mismatches:
Indels: -----PheGlnAlaGlyAspPro 195 -----GluGļYArgGļYAlaPro 146 ----SerGly 4135 455 129 254 140 316 140 140 388 83 78 196 136 72 763

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AHYTDVSNWGRARQKLAGRSWSVPITHLFAAPLKDYFACE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission Submission Submitted (17-MAY-1999) Department of Biochemistry and Molecular Submitted (17-MAY-1999) Department of Education of Basic Medical Sciences, Chinese Academy of Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005, P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'codon_start=1
'product="DNA cytosine-specific methyltransferase isoform
                                                                     Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 4278)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Mu, G.Y. and
Shen, Y.
                                                                                                                                                                       Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue Unpublished
Unpublished
Yin, E. (bases 1 to 4278)
Yin, E., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ProAlaMetProSer---SerGlyProGlyAspThrSerSers----AlaAlaGlu 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'function="methylates cytosine in DNA"
(note="alternatively spliced"
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Matches:
Conservative:
Mismatches:
Indels:
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59.24%
46.29%
                                                     Mus musculus.
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Query Match:
DB:
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  1889 CTGGAAGAATTTGAGCCACCCAAGTTGTACCCAGCAATTCCTGCAGAAAGGAGGCCC 1948
                                                                                                                                                                                                                                                                                                          2009 GGTATTAAAGTGGAAAAGTACATTGCCTCCGAAGTCTGTGCAGAGTCCATCGCTGTGGAA 2068
                                                                                                                                                                                                                                                                                                                                                                                                                                             2129 AATATTGAAGAGTGGGGCCCGTTCGACTTGGTGATTGGTGGAAGCCCATGCAATGATCTC 2188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2069 ACTGTTAAGCATGAAGGCCAGATCAAATATGTCAATGACGTCCGGAAAATCACCAAGAAA 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2369 GCATGTAACCCAGTGATGATGGATGCCATCAAGGTGTCTGCTGCTGCTCACAGGGCCCGGGTAC 2428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2429 TTCTGGGGTAACCTACCCGGAATGAACAGGCCCGTGATGGCTTCAAAGAATAAGATAAGCTC 2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2549 ACCACCAAGTCGAACTCCATCAGACAGGGCAAAAACCAGCTTTTCCCTGTAGTCATGAAT 2608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2609 GGCAAGGACGTTTTTGTGGTGCACTGAGCTCGAAAGGATCTTCGGCTTCCCTGCTCAC 2668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2669 TACACGGACGTGTCCAACATGGGCCGCGCGCCCGTCAGAAGCTGCTGGGCAGGTCCTGG 2728
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                                                                                                                                         615 --- GlnGluPheAspProProLysValTyrProProValProAlaGluLysArgLysPro 633
                                                                                                                                                                                                          634 IleArgValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLysAspLeu 653
                                                                                                                                                                                                                                                                                  GlylleGlnValAspArgTyrlleAlaSerGluValCysGluAspSer1leThrValGly 673
                                                                                                                                                                                                                                                                                                                                                     674 MetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValThrGlnLys 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheTyrargLeuLeuHisAspAlaArgProLysGluGlyAspAsgArgProPhePheTrp 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         774 GluSerAsnProValMetIleAspAlaLysGluValSerAlaAlaHisArgAlaArgTyr 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheTrpGlyAsnLeuProGlyMetAsnArgProLeuAlaSerThrValAsnAspLysLeu 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      814 GluLeuGlnGluCysLeuGluHisGlyArglleAlaLysPheSerLysValArgThrIle 833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    874 TyrThrAspValSerAsnMetSerArgLeuAlaArgGlnArgLeuLeuGlyArgSerTrp 893
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318 1184	298 YLYSLeuArgGlyPheSerTrpTrpProGlyArgIleVal8erTrpTrpMetThrGlyAr ::::: 	망양
298 1124	278 yAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuValTrpGl	B 6
278 1064	258 lAlaThrThrProGluProValGlySerAspAlaGlyAspLysAsnAlaThrLysAlaGl ::::	B 8
1004	::: ::: ::: :::	₽ 5
n un	CAGCGTCGACTT	₽ }
238	18 aLysVallleAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSerGlnLy	γ
906	::: ::: 91 GTCTCGGAGACGTCGA	ઠ
218	98 eSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLysAl	8
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189	159 GLEUATGGIYGLYLEUGLYITPGIUSETSETLEUATGGITATGPTOMETPTOATGLEUTTN	B &
770	1 GCCAAAGCTCACCCGTGAGACCAAGGACACCAGGACGCTCTGAAAGCCCGGCTGTCCG	D _D
169	rAsnIleGluSerMetLysMetGluGlySerArgGlyAr 	Ş
710	651 GACAGGAGATGGAGACAGAGATGATGATGATGATGGGGAATGGCTCTGATATTCTAAT	₽
149	rgGļķAlaProAlaGluAl	γQ
650	GTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACAT	В
140		δ
590	TGCACAGAGCCAGTCTGCACACCAGAGACCAGAGGCCGCAG	Db
140	roGluAlaSerArgAlaValGluAsnGlyCysCysThrProLysr	Ş
531		밁
125	roAlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLe	Ş
105 527	86 uLeuLeuProAsnGlyAspLeuGluLy8ArgSerGluProGlnProGlnGluGluGlySe	g oy
467	408 AACAATGAAGGGAGACAGCAGACATCTGAATGAAGAAGAGGGTGCCAGCGGGTATGAGGA	В
86	SerGlyAlaSerGl	Ş
407	348 GGGATCTCCCCCCCCATCCATAGTGCCTTGGGACCAAATCCAGGGCCTTCTTTCAGGA	B &
347	• CHRACTICALAMAGETITATACCTITAGAAACCTCAGGTATATACCTTTCCAGACGC	2
72	58 oProValGluSerGlyAspThrProLysAspProAlaValIle	3 8
287	CCTCACGA	ᅡ
58	38 gGlnGluProSerThrThrAlaArgLysValGlyArgProGlyArgLysArgLysHisPr	8

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676	2160	'n	636 2100	616 2040	597 1980	577 1920	557 1860	537 1800	517 1740	497 1680	477 1620	457 1569	437 1524	418 1464	398 1404	378 1365	358 1305	338 1245	318 1185
gHisGlnGlyLysIleMetTyrValGlyAspValArgSerValThrGlnLysHisIleGl 696	NALASPĀTGTYPILEĀLĀSETGLUVĀLCYSGLUĀSPŠGTLETHTVALGLYMETVALĀT 676 :::::		; lleuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLysAspLeuGlyIleGl 656 	UPHEASDPTOPTOLYSVAITYTPTOPTOValProAlaGluLySATGLYSPTOIleArgVa 63	ArgLeuGlnMetPhePheAlaAsnAsnHisAsp 	TyrMetCysGlyHisLysGlyThrTyrGlyLeu rarargrgccrcccrcAgcgcrgccArggggrc	alGlyProGlyAlaAlaG GGGCGCAGGCACAGCTGJ	GlyAsnAsnAsnC ::: AGTAACACAAGCT	:GlnTyrAspAspAspGlyTyr ::: ATGTATGATGAGGACGGCTAT	ThrLeuGluHisProLeuPheValGlyGly1 	rgGlnLysCysArgAsnIleGluAspIle ::: ccAacaacaaGGCAATCTGGAAGACCGG	OArgLysSerThrAlaGluLysProLysValLysGluIleIleAspO	PValGluProGluAlaAlaAlaTyrAlaProProProProAlaLysLysPr 4 GACTCTGCTGCTTCTGAGTCCCCCCCACCCAAGCGCCTCAA 1	yProLysGlyLeuGluProProGluG:	aValGluValGlnAsnLysProMetIleGluTrpAlaLeuGl:	rArgAlaGlyLysLeuPheProValCysHisAspSerAspGluSerAspThrAla TCGAGCTGGCAAGACCTTCTCCAGCAGTCCTGGA	rTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGlnVs -::: 	IValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPho	gSerArgAlaAlaGluGlyThrArgTrpVa

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A I CTEPUCTPETIRGRESSSRLSKREVSSLLNYTQDMTGDGDRDDEUDDRGSDILLMPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 -------LeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGlu 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 GluGlySerProAlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyAlaAla 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 ProSerThrThrAlaArgLysValGlyArgProGlyArgLysArgLysHisProProVal 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 LysSerProSerMetAlaGlnAspSer------GlyAlaSerGlu 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 TATGAGGAGTGCATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACGAT
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                                                                                                                                                                                               function="methylates cytosine in DNA"
note="alternatively spliced"
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Matches:
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/db_xref="GT.83.7.7
                             organism="Mus musculus"
strain="KM"
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AP151973 GI:8347127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue Unpublished
Unpublished
2 (bases 1 to 4223)
Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and
2280 AGAGTGGGGCCCGTTCGACTTGGTGATTGGTGGAAGCCCATGCAATGATCTCTCTAACGT 2339
                                                                                                                                                           2340 CAATCCTGCCCGCAAAGGTTTATATGAGGCACAGGAAGGCTCTTCTTCTTCGAGTTTTACCA 2399
                                                                                                                                                                                                                                          2400 CTTGCTGAATTATACCCGCCCCAAGGAGGCGACAACACCGTCCATTCTTCTGGATGTTCGA 2459
                                                                                                                                                                                                                                                                                                                     2460 GAATGTTGTGGCCATGAAAGGAATGACAAGAAAGACATCTCAAGATTCCTGGCATGTAA 2519
                                                                                                                                                                                                                                                                                                                                                                                                  2580 TAACCTACCCGGAATGAACAGGCCCGTGATGGCTTCAAAGAATGATAAGCTCGAGCTGCA 2639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2820 CGTGTCCAACATGGGCCGGGGCGCCGTCAGAAGCTGCTGGGGCAGGTCCTGGAGTGTACC 2879
                                                                                                                                       716 lAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrAr 736
                                                                                                                                                                                                               gLeuLeuHisAspAlaArgProLysGluGlyAspAspArgProPhePheTrpLeuPheGl 756
                                                          696 nGluTrpGlyProPheAspLeuVallleGlyGlySerProCysAsnAspLeuSerlleVa 716
                                                                                                                                                                                                                                                                                            uAsnValValAlaMetGlyValSerAspLysArgAspIleSerArgPheLeuGluSerAs 776
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15	Oy 396 AlaLysAlaValGluValGlnAsnLysDroMetIleGluTrpAlaLeuGlyGlyPheGln :::::::	
1280	1242 GCCAGGGTTCGAGCTGGCAAGACCTTCTCCAGCAGTCCT	н
395	76 AlaSerSerArgAlaGlyLysLeuPheProValCysHisAspSerAspGluSerAspThr	^
375 1241	OY 356 GINALETTETYASTIYEGINPROMECTYRARGIYEALILETYRGIUVALLEUGINVAL	
<u> </u>	336 PheSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPheHis	
1121	1062 ACCTCCAAGCGACAGGCCATGCCCGGAATGCGCTGGGTACAGTGGTTTGGTGATGGCAAG	-
335	SerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLys	_
315	296 ValTrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMet :::::	- 0
1001	942 AGCATATATGGAGACAGCACAGAGTATCAGGATGATAAAGAGTTTGGAATAGGTGACCTC	_
295	spGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeu	^
941	882 GTTGACTTGAGCCAGGATGGAGTCAGGAGGTGTATGGATACCACACAGGTGGATGCAGAG	-
275	FhrThrProGluProValGlySerAspAlaGlyAspLysAsnAlaThr	_
881	834 GTCGACTTCATGGAAGAGTGACACCTAAGAGCGTCAGTACCCCCATCA	н
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235	laGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGlu	0
791	768 GCTACCAGGTCTCGGAGACGTCGA	п
215	rLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGlu	_
767	708 AGAATCACCCGAGGTCGGCAGGGCCGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCG	п
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707	 	_
186	<pre>suhrqGlyGlyLeuGlyTrpGluSerSerLeuArqGlnArqProMetPro</pre>	_
647	Db 588 ATTCTAATGCCAAAGCTCACCCGTGAGACCAAGGACACCAGGACGCGCTCTGAAAGCCCCG	н
166	GluGlnLysGluThrAsnIleGluSerMetLysMetGluGlySer	0
587	: : : GAATGGCTĆTGAT	н
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Db 2517 TTCTGGGGTAACCTACCCGGAATGACAGGCCCGTGATGGCTTCAAAGAATGAT Qy 814 GluLeuGlnGluCysLeuGluHisGlyArgIleAlaLysPheSerLysValArg
SERBEPTOVALMELLEABBALALYSGULVALSER
754 LeuPheGluAsnValValAlaMetGlyValSerAspLysi :::
Qy 734 PheTyrArgLeuLeuHisAspAlaArgProLysGluGlyAs
Qy 714 SerIleValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhePhe
Qy 694 HisileGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCy ::: :::
Oy 674 MetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerVal ::: :::
Oy 654 GlylleGlnValAspArgTyrIleAlaSerGluValCysGluAspSo
IleAlaThrG ATTGCAACGG
15GlnGluPheAspProProLysValTy:
\langGluAspTrpProSerArgLeuGl\ ::: GAAAGATTGGAACATGCGCCTGCA
Qy 575 AlalleLysGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyrGl
/sValGluCysValAspLeuLeuVal #TGTGGAGTGTCTGGAGGTGCTGGTG
Qy 535 SerTyrCysThrIleCysCysGlyGlyArgGluValLeuMet(
Qy 515 GlnAsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAsp
95 Ilese ::: 17 TTGTC
Qy 475 ThrargGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGlv:::
55 LysLy ::: 06 CGCCT

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(Dnmt3b) mRNA,
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Okano, M., Chijiwa, T., Sasaki, H. and Li, E.
Direct Submissor.
Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
Sequence update by submitter
Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327979.
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Direct Submissor.
Submitted (28-MAY-1998) CYRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
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Okano, M., Xie, S. and Li, E.
Cloning and characterization of a family of novel mammalian DNA (cycosine-5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1999)
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Accession Numbers AA116694, AA119979, AA17277, AA210568,
AA407106, and AA575617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="de novo DNA methylation"
/note="alternatively spliced product; contains Cys-rich
region; C-terminal region is similar to corresponding
region of Max cytosine-5 methyltransferase 3A"
/codon_start=1
                                                                                           2637 ACCACCAAGTCGAACTCCATCAGACAGGGCAAAAACCAGCTTTTCCCTGTAGTCATGAAT 2696
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2757 TACACGGACGTGTCCAACATGGGCCGCGCGCCCCTCAGAAGCTGCTGGGCAGGTCCTGG 2816
                                                                                                                                                 854 GluLysGluAspIleLeuTrpCysThrGluMetGluArgValPheGlyPheProValHis 873
                                                                  834 ThrThrArgSerAsnSerIleLysGlnGlyLysAspGlnHisPheProValPheMetAsn 853
                                                                                                                                                                                                                                       TyrThrAspValSerAsnMetSerArgLeuAlaArgGlnArgLeuLeuGlyArgSerTrp 893
                                                                                                                                                                                                                                                                                                                                              2817 AGTGTACCGGTCATCAGACACCTGTTTGCCCCCTTGAAGGACTACTTTGCCTGT 2870
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/db_xref="GI:6449470"
                                                                                                                                                                                                                                                                                                                                                                                                                                                AF068626 4195 bp mRNA linear Mus musculus DNA cytosine-5 methyltransferase 3B1 alternatively spliced, complete cds.
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/db_xref="taxon:10090"
/chromosome="2"
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Matches:
Conservative:
Mismatches:
Indels: 950 t US-09-720-086-7 (1-912) x AF068626 (1-4195) 1059 c 1125 g 2.59e-80 2221.00 58.32% 45.69% Percent Similarity: Best Local Similarity: 1061 a Alignment Scores: Query Match: DB: BASE COUNT ORIGIN

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514	5 IleSerCysGlySerLeuAsnValThrLeuGluHisProLeuPheValGlyGlyMetCys	Оу 49
1588		Db 152
494	ArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAspIleCys	0у 47
in i	B CGCTCAAGACAAATAGCTATGGCGGGAAGGACCGAGGGGAGGATGAGGAG	147
J	5 LvsLvsProArgLvsSerT)	. 4. U
454 1477	5 ValTyrThrAspMetTrpV ::: 3 CGCACAACCAAT	Qy 43
40 (GTGCGTCGTTCAGACAGTAGGAACTTAGAACCCAGGAGACGCGAGAACAAAAGTCGAAGA	137
4 6		4 1
424 1372	6 ProSerGlyProLyBGlyLeuGluPro	Oy 41
415 1312	6 ALALYSALAVALGLUVALGLNASHLYSPYOMETILEGLUTYPALALEUGLYGLYPHEGIN ::::::::::	Qy 39 рь 125
1252	6 ALSGETSETATGALSGIYYSLEURPREPTOVALCYSHISASDSGTASDGIUSETASDIDT 	21.
N	4 CTGCTACCTTCAATAAGCTGGTTTCTTATAGGAAGGCCATGTACCACACTCTGGAGAAA	115
375	6 GlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGlnVal	0у 35
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> ⊢	GITGACTIGAGCCAGGAIGGAGAICAGGAGGTAIGGAIACCACAGGIGGAIGCAGAG	, a
275	6 ProThrValAlaThrThrProGluProValGlySerAspAlaGlyAspLysAsnAlaThr	25
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w	LysLysAlaLysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGlu	21
215 763	6 TyrTyrIleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGlu 2 	2y 196 0b 746
139 139	ArgLeuThr	Db 680
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Length:
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="DNA cytosine-specific methyltransferase isoform
                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                  (bases 1 to 4338)
(in, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                                             2 (bases 1 to 4338)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
Shen, Y.
                                    2729 TACACGGACGTGTCCCAACATGGGCCGCGCGCCCGTCAGAAGCTGCTGGGCAGGTCCTGG 2788
                                                                                                                                                                                                                                                                                  Cloning of full-length Dnmt3b cDNA and its alternative splicing
2669 GGCAAGGACGACGTTTTGTGGTGCACTGAGGTCGAAAGGATCTTCGGCTTCCTGCTGCTCAC 2728
                                                                                                               Mus musculus DNA cytosine-specific methyltransferase isoform 1 AF151969.1 GI:8347117
                      874 TyrThrAspValSerAsnMetSerArgLeuAlaArgGlnArgLeuGlyArgSerTrp 893
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/function="methylates cytosine in DNA"
/note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/dev_stage="8-9 day old embryo"
1. .4338
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                                                                                                                                                                                                                                                                                                in mouse embryonic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAF74515.1"
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                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Dnmt3b"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="KM"
                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                         Unpublished
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AF151969
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AUTHORS
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
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                                                                                                                                                                                           KEYWORDS
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Alignment Scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651 GACAGGAGATGGAGACAGAGATGAAGTAGATGGATGGGAATGGCTCTGATATTCTAAT 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 u---LeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGluGlySe 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 rProAlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLe 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 GGGATCTCCCCTCCCCATCCATAGTGCCTTGGGACCAAATCCAGGGCCTTCTTTCAGGA 407
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                                                                  2 ProAlaMetProSer---SerGlyProGlyAspThrSerSerSer----AlaAlaGlu 18
                                                                                                                                                                                                    19 -ArgGluGluAspArgLysAspGlyGluGluGluGluBroArgGlyLysGluGluAr 38
                                                                                                                                                                                                                                                                                                                                             38 gGlnGluProSerThrThrAlaArgLysValGlyArgProGlyArgLysArgLysHisPr 58
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288 CAGGCCGCTGAGGCTTGTGCCAGACCTTGGAAACCTCAGGTATATACCTTTCCAGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 p-----SerGlyAlaSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 GTGCATTATCGTTAATGGGAACTTCAGTGACCAGCACGAAGGATGCTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 ----SerLysSerProSerMetAlaGlnAs
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597	7 sGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgAr	57	ર્
1979	O CTTCTGTGGAGGTCTGGAGGTGCTGGTGGGCGCAGGCAGCTGAGGATGCCAAGCT	192	Д
577	7 sPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLy	55	Ş
<u>ن</u> و	O CACCGTGTGCTGTGAGGGCCGTGAACTGCTGCTGCAGTAACACAAGCTGCTGCAGATG		뮍
557	7 sThrIleCysCysGlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCy	53	Ş
537 1859	7 sLysasnCysPheLeuGluCysalaTyrGlnTyrAspAspAspGlyTyrGlnSerTyrCy ::::::	180	유 성
1799	TGGAAAGAAGAACCCTGTGTCCTTCCACCCCCTCTTTGAGGGTGGGCTCTGTCAGAGTTG	174	무 성
7	O ACGGATGGCTTCTGAAGTCACCAACAAGGGCAATCTGGAAGACCGCTGTTTGTCCTG	0 00	}
497	7 uArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAspIleCysIleSerCy	J	Ş
477 1679	7 OArgLysSerThrAlaGluLysProLysValLysGluIleIleAspGluArgThrArgGl	45 162	음 성
457 1628	aAlaAlaTyrAlaProProProProAlaLysLysPr acrectrotgagtcccccccccccAGCGCCTCAA	43	₽ <u>`</u> &
437 1583	ProGluGluGluLysAsnProTyrLysGluValTyrTh	42 152	P 6
1523	GATCGAGGGCTCAAACCCAACAAGAAGCAACCAGTGGTTAATAAGTCGAAGGTGCGTCG	6	В
424	8 yProLysGlyLeuGluPro	41	δ
418 1463	GlyPheGlnProSerGl ::: ::: GGCTTCAAGCCTACTGG	39 140	유 양
398 1403	yBHisAspSerAspGluSerAspThrAlaLysAl TCCAGCAGTCCTGGAGAGTC	37 136	망양
378 1364	B rTyrAsnLysGlnProMetTyrArgLysAlaTleTyrGluValLeuGlnValAlaSerSe :::	130	음 성
ا درا	GATCTCTGCTGACAAACTGGTGGCTCTGGGGGCTGTTCAGCCAGC	44.	Db ,
1244	TGCCCGGAATGCGCTGGTACAGTGGTTTGGTGATGGCAAGTTTTCTGA	33	ξ β ₋
338	SerhrgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLyspheSerVa	31	Ş
318 1184	rTrpTrpMetThrGlyAr ::	29 112	마 상
298 1124	GlyGluLeuValTrpGl ::: GTGACCTCGTGTGGGG	27 106	B 6
278 1064	BASDAlaThrLysAlaGl GATGCAGAGAGCATATA	25 100	음
258 1004	SValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerProThrVa	ώιω	음 성
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mRNA,	N Homo sapiens DNA cytosine methyltransferase 3 complete cds. AF331857	ore LL1
Į,	AF331857 4335 bp mRNA linear PRI	RESULT 14 AF331857 LOCUS
	OVALIIeArgHisLeuPheAlaProLeuLysGluTyrPheAlaCys 911	Qy 896 рь 2940
C 2939	PVALSETASIMETSETATGLEGGCGCCCGTCAGAAGCTGCTGGGCAGGTCCTGGAGTGTAC	Оу 876 Db 2880
28	cgacgTTTTGTGGTGCACTGAGCTCGAAAGGATCTTCGGCTTCCCTGCTCACTACACG	282
.s 876	uAspIleLeuTrpCysThrGluMetGluArgValPheGlyPheProValHisTyr	Оу 856
1 856 : A 2819	gSerAsnSerIleLysGlnGlyLysAspGlnHisPheProValPheMetAsnGluLysG:	Qy 836 Db 2760
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- Q-	CCAGTGATGATCGAGTGCCATCAAGGTGCTGCTTCTTTTTTTT	Db 2580
1 796	nProValMetIleAspAlaLysGluValSerAlaAlaHisArgAlaArgTyrPheTr	Qy 776
As 776 	uABNValValAlaMetGlyValSerAspLySArgAspIleSerArgPheLeuGluSer ABNTGTTGTGGCCATGAAAGTGACAAGAAAGACATCTCAAGATTCCTGGCATGT	Qy 756 Db 2520
11 756 - A 2519	GLeuLeuHisAspAlaArgProLysGluGlyAspAspArgProPhePheTrpLeuPheG	Qy 736 Db 2460
л 736 Э 2459	; lAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrA 	Qy 716 Db 2400
'a 716 T 2399	; nG1uTrpG1yProPheAspLeuVall1eG1yG1ySerProCysAsnAspLeuSerI1eV ;	Qy 696 Db 2340
1 696 : A 2339	GHisGlnGlyLysIleMetTyrValGlyAspValArgSerValThrGlnLysHisIleG 	Qy 676 Db 2280
Ar 676 :: 'AA 2279	nValAspArgTyrIleAlaSerGluValCysGluAspSerIleThrValGlyMetVal :::::	Qy 656 Db 2220
G1 656 :: 'AA 2219		Qy 636 Db 2160
ä 636 2159	uPheAspProProLysValTyrProProVall	Qy 616 Db 2100
1 616 A 2099	gArgGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsnHisAspGlnG ::: CAGGAAAGATTGGAACATGCGCCTGCAAGACTTCTTCACTACTGATCCTGAACCTGGAAG	Qy 597 Db 2040
G 2039	GCAGGAACCCTGGAGCTGCTATA	Db 1980

615

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1210 TCCTATCGAAAAGCCATGTACCATGCTCTGAAGAAAGCTAGGGTGCGAGCTGGGAAGACC 1269
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1150 CTGGTGGCACTGGGGCTGTTCAGCCAGCACTTTAATTTGGCCACCTTCAATAAGCTCGTC 1209
                                                                                                   283 CGCCCAGCCGCGCCCCAGCCAGCCAGGAAAGCATGAAGGGAGACACCAGGCAT 342
                                                                                                                                                              102 ------GlugluglySerProAlaglyGlnLys------GluglyGlyGlnLys-
                                                                                                                                                                                                                                                                 114 AlaProAlaGluGlyGluGlyAlaAlaGluThrLeuProGluAlaSerArgAlaValGlu 133
                                                                                                                                                                                                                                                                                                                                                                          134 AsnGlyCysCysThrProLys---GluGlyArgGlyAlaProAlaGluAlaGlyLysGlu 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 GAGGTGTCCAGTCTGCTAAGCTACACACAGGACTTGACAGGCGATGGCGACGGGGAAGAT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 -----LysGluThrAsnIleGluSer 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 MetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeu 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyrIleSerLys 200
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|704 AGGCCGCAACCATGTGGACGAGGACCAGGTTCCCGGCTACCAGGTCCCTGAGAC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 TyrGluAspGlyArgGlyPheGly1leGlyGluLeuValTrpGlyLysLeuArgGlyPhe 303
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223 CAGCGCCCTGCACGGCCGCCAGCCGGCCTCCCGCCAGCCCAGCCCCGACCCGGGCTCCGC 282
                                                    95 LysArgSerGluProGlnPro----- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 GlnGlnProThrAspProAlaSerProThrValAlaThr------ThrProGlu 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             875 GTACCCCCTACG---CCCGCCTAGCCCAGGACAGCCAGGAGGGGGCATGGAGTCCCGC 931
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                                                                                                                                                                                                397 GCTGCAGCGACCAGTCCTCCGACTCGCCCCCCAATCCTGGAGGCTATCGGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 556 GGGGATGGCTCTGACACCCCAGTCATGCCAAAGCTCTTCCGGGAAACCAGGACTCGTTCA
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/protein_id="AAL500.1"
/db_xref="G1:18033255"
/translation="MKGDTRHLNGEEDAGGREDSILVNGACSDQSSDSPPILEAIRTP
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4335) 101,J., Pradhan, S. and Roberts, R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 CTGGGGTTAAGTGGCCCAAGTAAACCTAGCTCGGCGATCGGCGCCGGAGATTCGCGAGGCC 222
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Cloning, erapression and characterization of human DNWT3 genes
Unpublished
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                                                                                                                                                                                                                                              2 (bases 1 to 4335)
Ni,J., Pradhan,S. and Roberts,R.J.
Direct Submission
Submitted (22-DEC-2000) New England Biolabs, 32 Tozer Road,
Beverly, MA 01915, USA
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            GlyGlySerProCysAsnAspLeuSerIleValAsnProAlaArgLysGlyLeuTyrGlu
                                                                                                          TGTGAGGAGTCCATTGCTGTTGGAACCGTGAAGCACGAGGGGAATATCAAATACGTGAAC
                                                                                                                              CysGluAspSerIleThrValGlyMetValArgHisGlnGlyLysIleMetTyrValGly
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CAGGCCTTCTTCACCAGTGACACGGGGCTTGAATATGAAGCCCCCAAGCTGTACCCTGCC
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1 (bases 1 to 4267)

Xu,G.-L., Bestor,T.H., Bourc'his,D., Hsieh,C.-L., Tommerup,N., Bugge,M., Hulten,M., Qu,X., Russo,J.J. and Viegas-Pequignot,E. Chromosome instability and immunodeficiency syndrome caused by mutations in a DNA methyltransferase gene mutations in a DNA methyltransferase gene 2 (bases 1 to 4267)

Xu,G.L. and Bestor,T.H.

Direct Submission
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/note="mutated in human chromosome instability and immundeficiency disease known as ICF syndrome; contains alternative 5' exon 1B" (codon, eterteit
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Matches:
Conservative:
Mismatches:
Indels:
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881 2706	862 ThrGluMetGluArgValPheGlyPheProValHisTyrThrAspValSerAsnMetSer	음 성
861 2646	842 GlnGlyLysAspGlnHisPheProValPheMetAsnGluLysGluAspIleLeuTrpCys	음 성
841 2586	822 GlyArgIleAlaLysPheSerLysValArgThrIleThrThrArgSerAsnSerIleLys	유 원
821 2526	802 AsnArgProLeuAlaSerThrValAsnAspLysLeuGluLeuGlnGluCysLeuGluHis	유 성
801 2466	782 AlaLysGluValSerAlaAlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGlyMet	참 칭
781 2406	762 GlyValSerAspLysArgAspIleSerArgPheLeuGluSerAsnProValMetIleAsp	B 8
761 2346	742 ArgProLysGluGlyAspAspArgProPhePheTrpLeuPheGluAsnValValAlamet	참 정
741 2286	722 GlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAla	B 성
721 2226	702 AspLeuVallleGlyGlySerProCysAsnAspLeuSerIleValAsnProAlaArgLys	참 중
701 2166	682 MetTyrValGlyAspValArgSerValThrGlnLysHisIleGlnGluTrpGlyProPhe	유 성
681 2106	662 AlaSerGluValCysGluAspSerIleThrValGlyMetValArgHisGlnGlyLysIle	음 정
661 2046	642 GlyIleAlaThrGlyLeuLeuValLeuLysAspLeuGlyIleGlnValAspArgTyrIle	β δ
641 1986	X22 ValTyrProProValProAlaGluLysArgLysProIleArgValLeuSerLeuPheAsp ::: :::	B 5
621 1926	602 ProSerArgLeuGlnMetPhePheAlaAsnAsnHisAspGlnGluPheAspProProLys	참 S
601 1866	582 AsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrp ::: 1807 AGCTGTTACATGTGTCTCCCGCAGCGCTGTCATGGCGTCCTGCGGCGCCGGAAGGACTGG	참 칭
581 1806	562 Cy8ValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrp	B 6
561 1746	542 GlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysDheCysValGlu 	음 성

Search completed: November 22, 2002, 10:57:33 Job time: 5471.49 secs

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Sequence 35, Appl
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Sequence 10, Appl
                                                                   US-09-248-335-53

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US-08-984-919A-12

US-08-781-420-10
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Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
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US-08-874-102-10

US-08-874-102-12

US-09-006-595A-10
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Sequence 10, Appl
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Patent No. 5340934
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Sequence 48, Appl
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Sequence 2, Appli
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US-09-344-441-2
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                                                                                                                               Sequence 11, Appl
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                                                                     US-09-032-684-11
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                    39.8
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ALIGNMENTS

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RESULT 1
US-09-276-531-47
Sequence 47, Application US/09276531
Patent No. 6183968
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Reddy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: 94304
COUNTE: CALIFORNIA
COUNTE: CALIFORNIA
COUNTE: CALIFORNIA
COUNTER: IBM PC COMPATION
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOO'R PEFFECE 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION:
APPLICATION NUMBER: 05/09/276,531
FILING DATE: Herewith
CLASSIFICATION
APPLICATION MUMBER: 42,918
REFERENCE/DOCKET NUMBER: 42,918
REFERENCE/DOCKET
LIBRARY. TESTITUTO2
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                                                                                3126 AAGATGGC---TTTCTTTTACCCTCCTGAGTTTATCACTC--AGAAGTGATGACTAAGAT 3180
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                                                                                                                                                                                                                                                                                                                                         484 GCTTTCCTGTGCACTACACAGACGTGTCCAACATGGGCCGTGGTGCCCGGCCAGAAGCTGC 543
3241 GTACTCAGGITCATGCTGCAAAATCACTTGAGATTTTGTTTTTAAGTAACCCGTGCTCCA 3300
                                                                                                                                               778
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                                                                   868
                                                                                                                                                                                                                                                                                                                                                    TTGCAGGGGAGCCCC--GGTGCTCCCTCCGTGTGCACAGCTCAGACCTGGCTGGCTTAGAG 3065
                                                                                                                                                                                                                                  CCCAGAGTCACCCTCCCTGAAGGCACCTCACCTGTCCCCTTTTTAGCTCACCTGTGTGG 2947
                                               AACGIGGCITTTTTTTTTTCCCCTTCCTGGGICTACCACTCAGAGAAACAATGGCTAAGAT 957
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1237 TTTCCACAATGATGATGATTTCAGCAGGGATGACGTCATCATC .1279	3474 CATTTCCCAGGATGATGTCAGCAGGGATGACATCACCACC 3515	1177 CGGCACATTCCCCTTGCCTAAATÄCÄÄÖĞĞTIKKÄĞTTCHGKACGGGACCTATTKGKGTAT 1234	OY - 3421 TGGCACCTTCCCCCTTCCCTTTGGTACAACGCCTGAAGTCCTGTTGGTCTTGTAG 3474	1125 TCGTTTTTTCCCAGGGCAAGCAGAAGAGAAAATGTTGTATATGTCTCTTTTACC 1176	3361 AAAAATTCCCCCCCCCCCCCAGGAGTATTTTGAAAGATGATGATGATTAAATTCTTTAAATTCTTTCC 54/60	TOTTTIACAGACGTGTGCAGTTGTAGGCATGTAGGCTACACAGAGATTTTTTAACGGCCAGGA	3301 CAPPTIGGTGGAGGATGGTATTTGTGAAATGTGAAAGTATGTAAAAAA	1918 GACAGTTATTGCAAGAGTTATTGAAAAGTTTTAAAAACTGCACTAATTGCTG 1664	
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
APPLICANT: Bandman
PLICANT: Lal, Pr.
LICANT: Hillman
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           PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: March 2:
CLASSIFICATION:
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ADDRESSEE: INCYTE PHARMACEUTICALS,
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                      APPLICANT: Guegier, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

TITLE OF INVENTION:—RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
TTORNEY/AGENT INFORMATION
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Lal, Preeti
Hillman, Jennifer
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                      UMBER: 60/079,677
March 27, 1998
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US-09-105-283-1
US-08-976-255-2
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US-08-971-15-537-3
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193, Appl
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TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: TESTTUTO2 CLOUE: 1271435 US-09-276-531-47
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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
597 GACTACTTTGCATGT
                                           903 GluTyrPheAlaCys 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 GCATCAAAGAATGATAAACTCGNGCTGCAGGACTGCTTGGAATACAATAGGATAGCCAAG
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                    AAGCTGCTGGGAAGGTCCTGGAGCGTGCCTGTCATCCGACACCTCTTCGCCCCCTCTGAAG
                                                                                                                                                                    ArgLeuLeuGlyArgSerTrpSerValProVall1leArgHisLeuPheAlaProLeuLys
                                                                                                                                                                                                                                                               NTCTTTGGCTTTCCTGTGCACTACACAGACGTGTCCAACATGGGCCGTGGTGCCCGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerThrValAsnAspLysLeuGluLeuGlnGluCysLeuGluHisGlyArgIleAlaLys 822
                                                                                                                                                                                                                                                                                                           ValPheGlyPheProValHisTyrThrAspValSerAsnMetSerArgLeuAlaArgGln
                                                                                                                                                                                                                                                                                                                                                                                                          CTTTTCCCTGTTGTCATGAATGGCAAAGAAGATGTTTNGTGGTGCACTGAGCTCGAAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGACCGGNCGTTCTTCTGGATGTTTGAGAATGTTGTAGNCTCGTGCCGATTCGGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrGlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAlaArgProLysGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGGCNANTGCAACGATCTNNAAAT-GTGAATCA-GCCAGGAAAGGCTGTATGAGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlySerProCysAsnAspLeuSerIleValAsnProAlaArgLysGlyLeuTyrGluGly 722
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UMBER: 42,918
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Mismatches:
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Matches:
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Minimum DB
Maximum DB
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Perfect score:
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17780.325 Million cell updates/sec
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1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

12.0 1050 22 AAH33850	17.7 4195 21 AAZ37096 14.3 709 24 ABQ57540	L AAZ37095 L ABL90391 L AAZ37098	9 Query Query Match Length DB ID D 99.8 4416 21 AAZ37097
	7096 DNA encoding de no 7540 Human colon cancer		ם

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ABK39945	ABV58336	ABV58007	ABL33032	AAS46704	ABL34072	ABQ67050	AAD28386	AAA10594	ABV58085	ABV61126	AA180464	AAI85778	ABL82861	ABL77340	AAH05250	ABS02382	AAI02414	AAI33860	AAI12506	AAK27928	AAK02490	ABA23961	ABA54212	ABA43755	AAC77455	AAF82964	AAI85785	AAS86166	ABA13731	ABA20255	ABL64228	ABN97389	AAT21884	AAF80537	AAS86165
Human chemically p	Human prostate exp	Human prostate exp	Human immune syste	Tumour suppressor	Human immune syste	Human angiogenesis	Human chemically t	Gene encoding a su	Human prostate exp	Human prostate exp	Human polynucleoti	Human polynucleoti		Human ovarian canc		Human genome-deriv	Probe #2405 used t	Probe #2546 used t	#2439		brain		foetal		ORFX ORF301	DNA methylt	Human polynucleoti	DNA encoding novel	Human nervous syst	Human nervous syst	Stomach cancer rel	Gene #3887 used to		Receptor #25 parti	DNA encoding novel

ALIGNMENTS

RESULT 1 AAZ37097

AAZ37097;

AAZ37097 standard; DNA;

4416 ВР

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CDS
                                                                                                                                                                 De novo DNA cytosine methyltransferase; DNMT3A; neoplastic disorder; carcinoma; sarcoma; leukaemia; DNA methylation; ss.
                                                                                                                                                                                                          27-MAR-2000
                      25-JUN-1998;
24-JUL-1998;
                                               25-JUN-1999;
                                                                29-DEC-1999.
                                                                                                                                                 Homo sapiens.
                                                                                                                                                                carcinoma; sarcoma; leukaemia; DNA methylation;
                                                                                                                                                                                         DNA encoding de novo DNA cytosine methyltransferase DNMT3A
                                                                                WO9967397-A1
      (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                          (first entry)
                      98US-0090906.
98US-0093993.
                                               99WO-US14373
                                                                                                                        Location/Qualifiers 353..3091
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New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias Okano M, Xie S; WPI; 2000-106298/09. P-PSDB; AAY54057. Ľi Ε,

Claim 10; Fig 1C; 114pp; English

The present sequence encodes a human de novo DNA cytosine methyltransferase designated DNWT3A. The polypeptides can be administered methyltransferase designated DNWT3A. The polypeptides can be administered therapeutically, especially by expressing encoding polynucleotides, too treat diseases associated with DNA cytosine methyltransferase, such as coplastic diseases associated with DNA cytosine methyltransferase, such as coplastic disorders, comeson to diseases, or determine susceptibility to neoplastic disorders, comeson for compounds inhibiting/accitabledy finds. They are useful to screen for compounds inhibiting/accitabledy companyabetide. The polypeptides can also be used for in vitro de novo repulate DNA such in vitro methylation may be used to direct or requiate DNA expression in biological systems, e.g. recombinant DNA complyation of DNA such in vitro methylated in vitro may be introduced into a cell/organism to increase or decrease expression of a desired polypeptide can also be complyated for which the native DNA is under-methylated or not methylated. The polypeptides can also be complyated in the produce antibodies which are useful to detect and purify the polypeptide or therapeutically e.g. to treat neoplastic disorders. The coplymolectides are useful to produce probes and primers which are considered and primers which are

Sequence 4416 BP; 1107 A; 1131 C; 1327 G; 851 T; 0 other;

184 ATCGAAGCCCCCACCCACACAGGCTGACAGAGGCACCGTTCACCAGAGGGCTCAACACACCGGG 243 GCCCTCCAGCGGCCCCGGGGACACCAGCAGCTCTGCTGCGGAGCGGGGAGGAGGACCGAAA 300 360 420 480 603 61 ATCGAAGCCCCCACCCACAGGCTGACAGAGGCACCGTTCACCAGAGGGCTCAACACCGGG 120 CAGCAGCCCCCCAGCCCCGCGCAGCCCCAGCCTGCCTCCCGGCGCCCCAGATGCCCGCCAT 240 363 423 483 543 0; Gaps 104 CAGCAGCCCCCAGCCCCCGCGCAGCCCCAGCCTGCCTCCCGGCGCCCCAGATGCCCGGCCAT 364 GCCTCCAGCGGCCCCGGGGACACCAGCAGCTCTGCTGCTGCGGAGCGGAGGAGGAGCGAAAA 424 GGACGGAGAGGAGGAGGAGGAGGAGGCCGCGTGGCAAGGAGGAGGGCCCAAGAGCCCAGCACCAC **GGACGGAGAGCAGCAGGAGCCGCGTGGCAAGGAGGAGCGCCAAGAGCCCCAGCACCAC** Query Match
99.8%; Score 4283.4; DB 21; Length 4416;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4287; Conservative 0; Mismatches 6; Indels 0; G 544 181 421 241 301 361 481 541 ò ò g 6 B 6 В g ò q q ò ò ò

QQ	664	GAGCCCTGCTGGGGGGCAGAAGGGCGGGGCCCCAGCAGAGGGAGAGGGTGCAGCTGAGAC 7	723
δ,	601		999
qa	724		783
ογ	661		720
qa	784	AGCCCCTGCAGAAGCGGGCAAAGAACAGAAGGAGCCAACAACATCGAATCCATGAAAATGGA E	343
δ	721		780
qq	844	GGGCTCCCGGGGCCGGCTGCGGGTGGCTTGGGCTGGGAGTCCAGCCTCCGTCAGCGGCC 5	903
ò	781	CATGCCGAGGCTCACCTTCCAGGGGGGACCCCTACTACATCAGCAAGGGGAAGGGGGA	340
q	904	CATECCGAGGCTCACCTTCCAGGCGGGGACCCCTACTACATCAGCAAGCGCAAGCGGGA 5	963
ογ	841	CGAGTGGCTGGCACGCTGGAAAAGGGAGCTGAGAAAAGCCAAGGTCATTGCAGGAAT \$	900
qq	964	CGAGTGGCTGGCAGCTGGAAAAGGGAGGCTGAGAAAGCCAAGGTCATTGCAGGAAT 1	1023
ò	901	GAATGCTGTGGAAGAAAACCAGGGGCCCGGGGAGTCTCAGAAGGTGGAGGAGGCCAGCCC 5	096
Db	1024	GAATGCTGTGGAAGAAAACCAGGGCCCGGGGAGTCTCACAAGGTGGAGGAGGCCAGCCC	1083
ò	196	TCCTGCTGTGCAGCAGCCCACTGACCCCGCATGTGGCTACCACGCCTGAGCC 1	1020
QQ	1084	TCCTGCTGTGCGCAGCCCCACTGACCCCCCACTGTGTGTG	1143
ò	1021	CGTGGGGTCCGATGCTGGGGACAAGGATGCCACCAAAGCAGCGGATGACGAGCCAGAGTA 1	1080
qq	1144	CGTGGGGTCCGATGCTGGGGACAAGAATGCCACCAAAGCAGGCGATGACGAGCCAGAGTA 1	1203
ò	1081	CGAGGACGGCCCGGGCTTTGGCATTGGGGAGCTGGTGTGGGGGAAACTGCGGGGCTTCTC	1140
qq	1204	CGAGGACGGCCGGGGCTTTGGCGATTGGGGGGGGGGGGG	1263
ò	1141	CTGGTGGCCAGGCCGCATTGTGTTGTGGATGACGGGCCGGAGCCGAGCAGCTGAAGG	1200
QQ	1264	CTGGTGGCCAGGCCGCATTGTGTCTTGGTGGATGACGGGCCGGAGCCGAGCTGAAGG	1323
ογ	1201	CACCCGCTGGGTCATGTGGTTCGGAGACGCAAATTCTCAGTGGTGTGTGT	1260
qa	1324	CACCCCTGGGTCATGTGGTTCGGAGACGGCAAATTCTCAGTGGTGTGTGT	1383
ò	1261	GATGCCGCTGAGCTCGTTTTGCAGTGCGTTCCACCAGGCCCACGTACAACAAGCAGCCCAT 1	1320
qq	1384	GATGCCGCTGAGCTCGTTTTGCAGTGCGTTCCACCAGGCCACGTACAACAAGCAGCCCAT 1	1443
ò	1321	GTACCGCAAAGCCATCTACGAGGTCCTGCAGGTGGCCAGCAGCGGCGGGGAAGCTGTT 1	1380
QQ	1444	GTACCGCAAAGCCATCTACGAGGTCCTGCAGGTGGCCAGCAGCCGCGGGGGAAGCTGTT 1	1503
ò	1381	CCCGGTGTGCCACGACAGCGATGAGAGTGACACTGCCAAGGCCGTGGAGGTGCAGAACAA 1	1440
qa	1504	CCCGGTGTCCCACGACAGCGATGAGAGACACTGCCAAGGCCGTGGAGGTGCAGAAAAA	1563
ò	1441	GCCCATGATTGAATGGGCCTGGGGGGTTCCAGCCTTCTGGCCCTAAAGGCCTTGAAGG	1500
qu	1564	GCCCATGATTGAATGGGCCCTGGGGGCTTCCAGCATTATGGCCCTAAGGGCCTGGAGCC	1623
ò	1501	ACCAGAAGAAGAGAAGAATCCCTACAAAGAAGTGTACACGGACATGTGGGTGG	1560
qg	1624	ACCAGAAGAAGAAGAATCCCTACAAAGAAGTGTACACGGACATGTGGGTGG	1683
δ	1561	GGCAGCTGCCTACGCACCTCCACCAGCAAAAAGCCCCGGAAGACACACAGCGGAGAAAAAA	1620
qo	1684	GGCAGCTGCATACGCACCACCTCCACCAGAAAAGCCCCGGAAGAGCACAGCGGAGAA 1	1743
ò	1621	GCCCAAGGTCAAGGAGATTATTGATGAGGGGCACAAGAGAGGGGGCTGGTGCTACGAGGTGGG	1680
qa	1744		1803

AGCCAAGTTCAGCAAAGTGAGGACCATTACTACGAGGTCAAACTCCCATAAAGCAGGGCAA 27 	TCAGCTGCACACAGGGCCCGCTACTTCTGGGGTAACCTT GCATCCACTGTGAATGATAAGCTGGAGCTGCAGGAGTGT 	TGACAAGAGGGACATCTCGCGATTTCTCGAGTCCAACCCTGTGATGATGATGATGACAAGA 2	461 GGAGGAGATGATCGCCCCTTCTTCTGGCTCTTTGAG	CCCAA 2	2341 GATTGGGGGCAGTCCCTGCAATGACCTTCTCCATCGTCAACCCTGCTCGCAAGGGCCTCTA 2400	2281 CGGGGACGTCCGCAGCGTCACACAGAAGCATATCCAGGAGTGGGGGCCCATTCGATCTGGT 2340	2221 GGTGTGAGGACTCCATCACGGTGGGCATGGTGCGGCACCAGGGGAAGATCATGTACGT 2280	2161 TACAGGGCTCCTGGTGCTGAAGGACTTGGGCATTCAGGTGGACCGCTACATTGCCTCCGA 2220	2101 ACCTGTCCCAGCTGAGAAGAGGAAGCCCATCCGGGTGCTGTCTCTCTTTGATGGAATCGC 2160	CAGGAATTTGACCCTCCAAAGGTTTACCC	TGCGGCGGCGAGAGGACTGGCCCTCCCG	1921 CCTCTTGGTGGGGCCGGGGGCTGCCCAGGCAGCATTAAGGAAGACCCCTGGAACTGCTA 1980	1861 TGAGGTGCTCATGTGCGGAAACAACAACTGCTGCAGGTGCTTTTGCGTGGAGTGTGTGA 1920	TACCAGTACGACGACGACGGCTACCAGTCCTACTGCACCATCTGCTGTGGGGGCCG 1	741 GGAACACCCCCTCTTCGTTGGAGGAATGTGCCAAAACTGCAAGAACTGCTTTCTGGAGTG 1	1681 GCAGAAGTGCCGGAACATTGAGGACATCTGCATCTCCTGTGGGAGCCTCAATGTTACCCT 1740
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Qy D5 Qy	Db Db	Db Oy Db	원 문 원 -	da Vo	D 09	d da	. B. 8	B Q	B 29	B 03	DP QA	Db. Qy	B Q	g Qy	g Qy	д Qy
37 38	37	37	ա ա u	ω ω 4 0 1	ω ω 5 4	ω w	υ υ υ 4. υ	y 324 b 336	w w	32	31	y 3001 b 3124	ωκ	30	2 2 8	y 2761 b 2884
81 TGAGATATATATAAAAGGTACTGTTAACTACTGTACAACCCGACTTCATAATGGTGCT	1 AATCA 4 AATCA	4 4	1 GGGAC 4 GGGAC	TTTTT	21 GAAATCTATATATTGGGTTGTTTTTTTTTTGTTTTTTTTT	ATAGT/ ATAGT/	1 TITIG	1 TTTTT 4 TTTTT	1 TATTC	1 AATAC 4 AATAC	1 AGAGA 4 AGAGA)1 ARGTTAARCAAACAAACAAAAAACACAAAACATAATAAACACCAAGAACATGAGGATGG 	GCTGA GCTGA	GAGGC GAGGC	21 GGAAAGGGTATTTGGTTTCCCAGTCCACTATACTGACGTCTCCAACATGAGCCGCTTGG 	31 AGACCAGCATTTTCCTGTCTTCATGAATGAGAAAAGAGGACATCTTATGGTGCACTGAAAT

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4140
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3964 TTCAAACAGCGAGATGAGTAAAACATCAGCTTCCACGTTGCCTTCTGCGCAAGGGTTT 4023
                                                                                                                                                                                                                                                           4264 ACGGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGAGGGCTCCTTGTGGGAT 4323
                                                                                                                                                                                                                                                                                          CAGAACTAATCCAGAGTGTGGGAAAGTGACAGTCAAAACCCCACCTGGAGCAAATAAAAA 4260
                                                                                                                                                                                                                                                                                                          De novo DNA cytosine methyltransferase; Dnmt3a; neoplastic disorder; carcinoma; sarcoma; leukaemia; DNA methylation; ss.
                                                       4024 CACCAAGGATGGAGAAAGGGAGACCTTGCAGATGGCGCGTTCTCACGGTGGGCTCTTC
                                                                                                       4084 CCCTTGGTTTGTAACGAAGTGAAGGAGAGAACTTGGGAGCCAGGTTCTCCCTGCCAAAA
                                                                                                                                                       4204 ATGCAATAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCTCGGCAAGATGGCAGAGGT
                                       CACCAAGGATGGAGAAAGGGAGACAGCTTGCAGATGGCGCGTTCTCACGGTGGGCTCTTC
                                                                                        CCCTTGGTTTGTAACGAAGTGAAGGAGAGAACTTGGGAGCCAGGTTCTCCCTGCCAAAA
                                                                                                                                       AGGGGGCTAGATGAGGTGGTCGGGCCCGTGGACAGCTGAGAGTGGGATTCATCCAGACTC
                                                                                                                                                                                                                                          4141 ACGGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGAGGGCTCCTTGTGGGGAT
                                                                                                                                                                                        ATGCAATAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCTCGGCAAGATGGCAGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "de novo DNA cytosine methyltransferase Dnmt3a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding de novo DNA cytosine methyltransferase Dnmt3a.
                                                                                                                                                                                                                                                                                                                                            4261 AACATACAAAACGTAAAAAAAAAAAAAAAAA 4293
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
217..2943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 1A; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ37095 standard; DNA; 4192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-106298/09.
P-PSDB; AAY54055.
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The present sequence encodes a murine de novo DNA cytosine methyltransferase designated bomuta. The polypeptides can be administered therapeutically, especially by expressing encoding polymucleotides, to treat diseases associated with DNA cytosine methyltransferase, such as neoplastic disorders e.g. carcinomas, sarcomes and leukemias. They can be used to disgnose, or determine susceptibility to neoplastic disorders, by assaying for polypeptide expression levels in mammalian cells/body fluids. They are useful to screen for compounds inhibiting/activating the polypeptide. The polypeptides can also be used for in vitro de novo methylation of DNA. Such in vitro methylation may be used to direct or regulate DNA expression in biological systems, e.g. recombinant DNA methylated in vitro may be introduced into a cell/organism to increase or decrease expression of a desired polypeptide for which the native DNA is under-methylated or not methylated. The polypeptides can also be used to produce antibodies which are useful to detect and purify the polypeptide or therapeutically e.g. to treat neoplastic disorders. The polymolectides are useful to produce probes and primers which are useful diagnostically.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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1702 AGGEATGTGCCAGAACTGCTAAGAACTGCTTCTTGGAGTGTGCGTACCAGTACGACGACGA 1821 1737 AGGCATGTGCCAGAACTGTAAGAACTGCTTCTTGGAGTGTGCTTACCAGTATGACGACGA 1796	702 GGACATCTGCATCTCCTGTGGGAGCCTCAATGTTACCCTGGAACACCCCCTCTTCGTTGG 17	н н	TTAT 164	1522 CTACAAAGAAGTGTACACGGACATGTGGGTGGAACCTGAGGCAGCTGCCTACGCACCACC 1581	ATCC 152	146		ACCGCAAAGCCATCTACGA 134 ACCGCAAAGCCATCTACGA 131	TTTG 128	1162 GTCTTGGTGGATGACGGGCCGGAGCCGAGCAGCTGAAGGCACCCGCTGGGTCATGTGGTT 1221	116 113	CAAGAATGCCACCAAAGCAGGCGATGACGAGCCAGAGTACGAGGACGGCCGGGGCTTTGG	TGACCCCGCATCCCCCACTGTGGCTACCACGCCTGAGCCCGGTGGGGTCCGATGCTGGGGA	GGGGCCCGGGGAGTCTCAGAAGGTGGAGGAGGCCAGCCCTCCTGCTGTGCAGCAGCCCAC	AAGGGAGGCTGAGAAGAAAGCCAAGGTCATTGCAGGAATGAAT	gggggggacccctactacatcagcaagcgcaagcgggacgaggtggctggc	742 GGGTGGCTTGGGCTGGGAGGTCCAGCCTCCGTCAGCGGCCCATGCCGAGGCTCACCTTCCA 801
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817 902	782 CATGA	722 GACCATTACTACGACGTCAAACTCCATAAAGCAGGGCAAAGACCAGCATTTTCCTGTCTT	1662 TAAGCTGGAGCTGCAGGAGTGTCTGGAGCATGGCAGAGATAGCCAAGTTCAGCAAAGTGAG 2721	:602 CCGCTACTTCTGGGGTAACCTTCCCGGTATGAACAGGCCGTTGGCATCCACTGTGAATGA 2661 	1942 ATTTCTCGAGTCCAACCCTGTGATGATTGATGCCAAAGAAGTGTCAGCTGCACACAGGGC 2601 	2482 CTTCTGGCTCTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCGCG 2541	2422 CTTTGAGTTCTACCGCCTCCTGCATGATGCGCGGGCCCAAGGAGGAGGAGATGATCGCCCCTT 2481	362 TGACCTCTCCATCGTCAACCCTGCTCGCAAGGGCCTCTACGAGGGCACTGGCCGGCTCTT 2421	2302 ACAGAAGCATATCCAGGAGTGGGGCCCATTCGATCTGGTGATTGGGGGCAGTCCCTGCAA 2361 	242 GGTGG 217 GGTGG	2182 GGACTTGGGCATTCAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATCAC 2241	2122 GAAGCCCATCCGGGTGCTGCTCTCTTTGATGGAATCGCTACAGGGCTCCTGGTGCTGAA 2181	2062 TAACCACGACCAGGAATTTGACCCTCCAAAGGTTTACCCACCTGTCCCAGCTGAGAAGAG 2121	2002 CTACGGGCTGCTGCGGCGGCGAGAGGACTGGCCCTCCCGGCTCCAGATGTTCTTCGCTAA 2061	.942 TGCCCAGGCAGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCACAAGGGTAC 2001 	.882 CAACAACTGCTGCAGGTGCTTTTGCGTGGAGTGTGGACCTCTTGGTGGGGCCGGGGGC 1941 	.822 CGGCTACCAGTCCTACTGCACCATCTGCTGGGGGGCCGTGAGGTGCTCATGTGCGGAAA 1881

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3114 GCTTGGCCTTGCAAAAGGGTTGGACATCATCTCCCTGAGTTTTCAATGTTAACCTTCAGTC
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                                 2962 TGTGTAAGGGACATGGGGGCAAACTGAGGTAGCGA----CACAAAGTTAAACAAACAAAC
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; antiorouvulaent; antidacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                           3949 TCAGCTGAGGTGGTCGGACCTGGGGAAGCTGAGTGTGGAATTTATCCAGACTCGCGTG 4008
                                                                                                                                                                                                         4027 CTAGATGAGGTGGTCGGCCCCGTGGACAGCTGAGAGTGGGATTCATCCAGACTCATGCAA 4086
                                                                                                                                                                                            4264
3902 ACCCCCCACAAAAAGGGGC 3948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders
                                                                                               4009 AATAACCTTAGAATATGAATCTAAAATGACTGCCTCAGAAAAATGGC-----TTGAGAA
                                                                               4087 TAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCTCGGCAAGATGGCAGAGGGTACGGAG
                                                                                                                                     4147 TCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGAGGCCTCCTTGTGGTGGGATCAGAAC
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                                                                                                                                                                                            TAATCCAGAGTGTGGGAAAGTGACAGTCAA--AACCCCACCTGGAGCAAATAAAAAAAAA
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P-PSDB; ABB89982.
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or uroganical; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

Claim 4; SEQ ID NO 953; 2081pp + Sequence Listing; English.

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Best Local Similarity
Matches 2781; Conserv
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Note: The sequence data for this patent did not form part of the
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TATCCAGGAGTGGGGCCCATTCGATCTGGTGATTGGGGGCAGTCCCTGCAATGACCTCTC
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3391 GGAGGAGAGGAAAAAAGGGAAATT	3331 GGTTATTGCAGCAAAATCAGTAACAAAAAATAGTAACAATACCTTGCAGAGG 	3271 CTTTTCAGAGGGGTTTTCTGTTTGGTTTTGGTTTTGTTTCTTGCTGTG	3211 AAGCTCCCTTCCCTTCCCCCTTCCCTTTTTTTTTTTTTT	3151 GTTGGACATCATCTCCTGATTTTTCAATGTTATTCTTCAGTCCTATTTAAAAA(3091 GGAATTTAAAACAAAACCACAGAGGGGAAATACCGGAGGGCTTTGCCTTGCC 	3031 CATAATAAAACACCAAGAACATGAGGATGGAGAGAGTATCAGCACCCAGAAGAC 	2971 GACATGGGGGCAAACTGAGGTAGCGACACAAAGTTAAACAAAC	2911 CGTGCCAGTCATCCGCCACCTCTTCGCTCCGCTGAAGGAGTATTTTG	2851 TACTGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGGTC	2791 GAAAGAGGACATCTTATGGTGCACTGAAATGGA 	2731 TACGAGGTCAAACTCCATAAAGCAGGGCAAAGACCAGCATTTTCCTGTCTTCAT	2671 GCTGCAGGAGTGTCTGGAGCATGGCAGGATAGCCAAGTTCAGCAAAGTGAGGAC 	2611 CTGGGGTAACCTTCCCGGTATGAACAGGCCGTTGGCATCCACTG	2551 GTCCAACCCTGTGATGATTGATGCCAAAGAAGTGTCAGCTGCACACAGGGCCCG	2491 CTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACA:	2431 CTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGAGATGATCGCCCCTT	2371 CATCGTCAACCCTGCTCGCAAGGGCCTCTACGAGGGCACTGGCCC	849 TATCCAGGAGTGGGGCCCATTCGATCTGGTGATTGGGGGCAGTCCCTGCAA
TTTTT 3	HAAAGGTG 3	AAGAA 1	CTACT 3	CAAAACC 3	4141	5-5			(2—C)	CACTA 2	ATGA ATGA	ი—ი	CTGGA 2	CTACTT	CTCGA	TGGCT	111	CTCTC 9
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24-JUL-1998;
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AACTGGTGGCACTGGGGGTTCAGCCAGCACTTTAATTTGGCCACCTTCAATAAGCTCG
                                                             AGCTGATGCCGCTGAGCTCGTTTTGCAGTGCGTTCCACCAGGCCACGTACAACAAGCAGC 1316
                                                                                                                                                                                                                                                                             TCTCCTGGTGGCCCGCCATGGTGGTGTCTTGGAAGGCCACCTCCAAGCGACAGGCTATGT
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Pred. No. 1e-145;
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/product= "de novo DNA cytosine methyltransferase
| Dnmt3bl"
                                                                                            2432 TACCGCCTCCTGCATGATGCGCGCCCAAGGAGGGAGATGATCGCCCCTTCTTCTGGCTC
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The present sequence encodes a murine de novo DNA cytosine
methyltransferase designated Dnmt3b1. The Dnmt3b gene also produces,
through alternate splicing, at least two shorter isoforms of 840 and
through alternate splicing, at least two shorter isoforms of 840 and
through alternate splicing, at least two shorter isoforms of 840 and
to given in the specification). The polypeptides can be administered
the appearance of the specification of the polypeptides can be administered
the specially by expressing encoding polynucleotides, to
therapeutically, especially by expressing encoding polynucleotides, to
therapeutically, especially by expressing encoding polynucleotides, to
therapeutically, especially by expressing encoding polynucleotides, uch as
neoplastic disorders e.g. carcinomas, sarcomas and leukemias. They can
be used to disorperide expression levels in mammalian cells/body
fluids. They are useful to screen for compounds inhibiting/activating the
polypeptide. The polypeptides can also be used for in vitro de novo
methylated in vitro may be introduced into a cell/organism to increase
or decrease expression of a desired polypeptide can also be
thylated to therapeutically are useful to detect and purify the
polypeptide or therapeutically e.g. to treat neoplastic disorders. The
polypeptide are useful to produce probes and primers which are
considered to produce antibodies which are useful to detect and purify the
polypeptide or therapeutically e.g. to treat neoplastic disorders. The
cuseful disgnostically.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 4195;
                                                                                              New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
17.7%; Score 760.4; DB 21; Length 4
Best Local Similarity 63.7%; Pred. No. 6.8e-145;
Matches 1270; Conservative 0; Mismatches 661; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4195 BP; 1061 A; 1059 C; 1123 G; 952 T; 0 other;
                                                                                                                                                                                Claim 9; Fig 1B; 114pp; English.
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample

New isolated nucleic acid that is differentially expressed it tissues useful for determining the presence of colon cancer or tissue type, and in antisense therapy.

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2002-426115/45

Claim

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A AH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where cancer-associated nucleic acid molecules (N) and proteins. The colon cancer antigens have cytostatic activity and can be used in gene cancer antigens have cytostatic activity and can be used in gene cherapy and vaccine production. N and P may be used in the prevention, changoosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient of separate and activity of P by expressing contains a patient of separate and activity of P by expressing P inactive proteins or to supplement the patients own production of P additionally. N may be used to produce the colon cancer-associated PB, by inscriting the nucleic acids into a host cell and culturing the cell and treatment of colorectal carcinomas and cancers. AH37196 to AH37204 and treatment of colorectal carcinomas and cancers. AH37196 to AH37204 present invention.

N IB Pages 66 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for expressing the interior.

SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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  Human, colon cancer, colon cancer antigen; diagnosis; detection;
colorectal carcinoma; ss.
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of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
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14.3%; Score 613; DB 24; Length 709;
Best Local Similarity 94.5%; Pred. No. 3.6e-115;
Matches 664; Conservative 0; Mismatches 33; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                               1 GGACGTCGGGGACGTCCGCAGCGTCACAAACATATCCAGGAGTGGGGGCCCATTCGA 60
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                                                                                                                                                                         Sequence 709 BP; 163 A; 177 C; 193 G; 168 T; 8 other;
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the Invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1951 AGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCACAAGGGTACCTACGGGCT 2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1651 CACAAGAGAGGGGCTGGTGTACGAGGTGCGGCAGAAGTGCCGGAACATTGAGGACATCTG 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1711 CATCTCCTGTGGGAGCCTCAATGTTACCCTGGAACACCCCCTCTTCGTTGGAGGAATGTG 1770
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                                                                                                                                                                                                                             1471 CCAGCCTTCTGGCCCTAAGGGCCTGGAGCCACCAGAAGAAGAAGAAGAATCCCTACAAAGA 1530
                                                                                                                                                                                                                                                                                                         1531 AGTGTACACGGACATGTGGGAACCTGAGGCAGCTGCCTACGCACCACCTCCACCAGC 1590
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                                                                                                                                                                                                                                                                                                                                                                                                                     122 CAAAAAGCCCCGGAAGAGCACAGCGGAGAAGCCCCAAGGTCAAGGAGATTATTGATGAGCG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 CTGCAGGTGCTTTTGCGTGGAGTGTGTGGACCTCTTGGTGGGGCCCGGGGGCTG-GCAAGC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 AGTGTACACGGACATGTGGGTGGAACCTGAGGCAGCTGCCTACGCACCTYCACCAGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 GTCCTACTGCACCATCTGCTGTGGGGGCCGTGAGGTGCTCTGTGTGCGGGAAACAACAACAG 421
                                                                                                                                        Ouery Match 11.8%; Score 504.6; DB 22; Length 622; Best Local Similarity 98.0%; Pred. No. 4.1e-93; Matches 540; Conservative 2; Mismatches 6; Indels 3; Gaps
                                                                                                                                                                                                                                                     2 CCAGCCTTCTGGCCCTAAGGGCCTAGAGCCACCAGAAGAAGAAGAAGAATCCCTACAAAGA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 CACAAGAGGGGCTGGTGACGAGGTGCGGCAGAAGTGCCGGAACATTGAGGACATTTG
                                                                                                     Sequence 622 BP; 154 A; 161 C; 189 G; 112 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA sequence SEQ ID NO:11099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH14009 standard; cDNA; 3017 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0248036.
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is used in preventing, treating or ameliorating a medical condition -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 272; 1297pp + Sequence Listing; English.
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13-OCT-2000; 2000US-0239935.
13-OCT-2000; 2000US-0229937.
20-OCT-2000; 2000US-024937.
20-OCT-2000; 2000US-0241221.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241786.
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20-OCT-2000; 2000US-0246524.
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20-OCT-2000; 2000US-0246209.
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17-NOV-2000; 2000US-0249212.
17-NOV-2000; 2000US-0249213.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249216.
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06-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
11 DEC-2000; 2000US-0251999.
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P-PSDB; AAM94301.
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Ota T,
Ishii S,
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11-JAN-2000; 2000UP-0118776.
02-MAY-2000; 2000UP-0183767.
09-JUN-2000; 2000UP-0241899.
WPI; 2001-318749/34.
                                                                                                       (HELI-) HELIX RES INST.
                                    Isogai T, Nishikawa T, Hayashi K, S, Sugiyama T, Wakamatsu A, Nagai K,
                                         Saito K, Y
, Otsuki T;
                                                            Yamamoto J;
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

Claim 8; SEQ ID 11099; 2537pp + CD ROM; English

complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as as ily without any specialized methods. AAH03166 to AAH33628 and AAH431671 The AAH43673 The primers allow obtaining of the full-length cDNAs as a sily without any specialized methods. AAH03166 to AAH33628 and The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification the present invention. an oligonucleotide comprising a sequence complementary to the exemplification

Sequence 3017 BP; 749 A; 751 C; 760 G; 757 T; 0 other;

DB 22; Length 3017;

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 1573 CGCACCACCACCAGCCAAAAAGCCCCGGAAGAGCACAGCGGAGAAGCCCAAGGTCAA 1632
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                                                            AAGGCCGTGGAGGTGCAGAACAA----GCCCATGATTGAATGGGCCCTGGGGGGCTTCCA 1473
                                                                                                                                                                                                                                                                                                        GCCACGTACAACAAGCAGCCCATGTACCGCAAAGCCATCTACGAGGTCCTGCAGGTGGCC 1357
                                                                                           AAGCCCATGTTGGAGTGGGCCCACGGGGCTTCAAGCCCACTGGGATCGAGGGCCTCAAA 240
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Pred. No. 2.5e-90;
0; Mismatches 548
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2653 TGTGAATGATA 2663 	Qγ
2593 ACACAGGGCCCGCTACTTCTGGGGTAACCTTCCCGGTATGAACAGGCCGTTGGCATCCAC 2	4G 4O
2533 CATTTCGCGATTTCTCGAGTCCAACCCTGTGATGATTGAT	B 5
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CGGCTCTTCTTCGAATTTTACCACCTGCTGATTACTCACGCCCCCAAGGAGGTGA CGCCCCTTCTTCTGGCTCTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAG	
413 CCGGCTCTTCTTTGAGTTCTACCGCCTCCTGCATGATGCGCGGGCCCAAGGAGGGAG	\$ \display
2353 TOCONGCARTGACCTOTCCARTOGTCARCCCTGCTCGCARAGGCCTCTACGAGGGCACTGG 24	유 성
080 GAACATCACAAAGAAAATATTGAAGAATGGGGCCCATTTGACTTGGTGATTGGCGGAAG	망
GGGCCCATTCGATCTGGTG	δ
2233 CTCCATCACGGTGGGCATGGTGCGGCACCACGGGGAAGATCATGTACGTCGGGGACGTCCG 22	유 성
960 AGTCCTCAAAGAGTTGGGCATAAAGGTAGGAAAGTACGTCGCTTCTGAAGTGTGTGAGGA	망
rggaccgctacattgcctcggaggtgtgtga	Ş
2113 TGAGAAGAGGAAGCCCATCCGGGTGCTGTCTTCTTTGATGGCATCGCGACAGGCTACCT 95	용 성
840 CTTCACCAGTGGCACGGGGCTTGAATACGAAGCCCCCAAGCTGTACCCTGCCATACCCGC	망
2053 CTTCGCTAATAACCACGACCAGGAATTTGACCCTCCAAAGGTTTACCCACCTGTCCCAGC 21	Ş
780 GCAGCGCTGTCATGGCGTCCTGCGGCGCCGGAAGGACTGGAACGTGCGCCTGCAGGCCTT B	B 4
93 CARRIAGENACCIONISCONTOCONTOCONTOCONTOCONTOCONTOCONTOCONT	2 6
1933 GCCGGGGGCTGCCCAGGCAGTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCA 19	B 8
660 TIGCAGCAACACGAGCTGCTGCCGGTGTTTCTGTGTGGAGTGCCTGGAGGTGCTGGTGGG 71	밁
1873 GTGCGGAAACAACAGCTGCTGCAGGTGCTTTTGCGTGGAGTGTGTGGACCTCTTGGTGGG 19	Ş
600 TGATGACGATGGCTATCAGTCTTACTGCACTGTGTGCTGCGAGGGCCGAGAGCTGCTGCT	B K
1813 CGANGANGANGGANTAN TITITANAN TANAN TANAN TANAN TANAN TANAN TITITAN TITITAN TITITAN TITITAN TITITAN TANAN T	§ §
3 CTTCGTTGGAGGAATGTGCCAAAACTGCAAGAACTGCTTTCTGGAGTGTGCGTACCAGTA 1	3 5
480 CAGCCTGGAAGATGGCTGTTTGTCTTGTGGCAGGAAAAACCCCGTGTCCTTCCACCCTCT 53	뮍
1693 GAACATTGAGGACATCTGCATCTCCTGTGGGAGCCTCAATGTTACCCCTGGAACACCCCCT 17	Ş
0 CCGAGGGGATGAAGATCAGAAGCCGAGAACAAATGGCTTCAGATGTTGCCCAACAAGAG 4	망
3 GGAGATTATTGATGAGCGCACAAGAGAGCGGCTGGTGTACGAGGTGCG	γ <u>ο</u>
360 CTCTGACTACTGCCCCGCACCCAAGGCCCCAAGGACAAATTGCTATAACAACGGCAAAGA 41	뫄

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Composition having probes which comprise part of gene sequence encoding proteins associated with cell proliferation useful as hybridizable array elements in Microarrays to monitor expression of target polynucleotide
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                                                                                              2255 CGGCACCAGGGGAAGATCATGTACGTCGGGGACGTCCGCAGCGTCACACAGAAGCATATC 2314
                                                                                                                                                                                            2315 CAGGAGTGGGGCCCATTCGATCTGGTGATTGGGGGCAGTCCCTGCAATGACCTCTCCATC 2374
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                           61 AAGGTAGGAAAGTACGCTTCTGAAGTGTGTGGAGGAGTCCATTGCTGTTGGAACCGTG 120
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2195 CAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATCACGGTGGCCATGGTG
                                                                                                                                                                                                                                                                                       2375 GTCAACCCTGCTCGCAAGGGCCTCTACGAGGGCACTGGCCGGCTCTTCTTTGAGTTCTAC
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Baughn MR;
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Specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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8.0%; Score 344.2; DB 23; Length
Best Local Similarity 75.0%; Pred. No. 2e-60;
Matches 430; Conservative 0; Mismatches 143; Indels
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                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #21969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo int/pub/published_pct_sequences.
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                                                                                                                         AASB6165 standard; cDNA; 711 BP.
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23-AUG-2000; 2000US-0649167.
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     1440 TGTGCACTACA 1450
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P-PSDB; ABG21978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2412 GCCGGCTCTTCTTTGAGTTCTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGAGGAAATG 2471
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  14-AUG-1996
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les 416; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCTGTTGTCATGAATGGCAAAGAAGATGTTTNGTGGTGCACTGAGCTCGAAAGGNTCT
                                                                                                            standard; cDNA to mRNA; 301
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Pred. No. 3e-56;
0; Mismatches 1
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                                                                                                            BP
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Best Local Sim.
Matches 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                 A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (cene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-c untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be gequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                            3579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                               3759
                                                                                              3699
                                                                                                                                                          3639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying gene signatures in 3'-directed human cDNA library - e. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                          3519 GATCAGATAGGAGCACAAGCAGGGGACGGAAAGAGAGACACTCAGGCGGCAGCATTCC
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 301 BP; 96 A; 65 C; 63 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 991-992; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                       recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                               181
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241
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                                                                                                                                                                                                                                                          <u>بــ</u>
                                                                                                                                                                                                                CTCCCAGCCACTGAGCTGTCGTGCCAGCACCATTCCTGGTCACGCAAAACAGAACCCCAGT
                                                                                                                                                                                                                                                            GTTTATATATATATAGATAGATATGNGNTATATATATAAAAGGTACTGTTAACTACTGTAA
                  CCACACAGGAAACCTTGAAGAAAATCAGTTTCTAGAAGCCGCTGTTACCTTGTTTACA 3758
                                                                                                                            TAGCAGCAGGAGACGAGACACCACACAAGACATTTTTCTACAGTATTTCAGGTGCCTA 180
                                                                                                                                                         TAGCAGCAGGAGAGACGAGAACACCACAAGACATTTTTCTACAGTATTTCAGGTGCCTA 3698
                                                                                                                                                                                          CTNCCAGCCACTGAGCTGNCGTGCCAGCACCATTCCTGGTCACGCAAAACAGAACCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene signature HUMGS03426
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                      6.6%;
                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                       Score 285.2; DB 16;
Pred. No. 1.5e-48;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                       66 T; 11 other;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                         301;
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Human, cancer, colon, breast, ovary, oesophagus, kidney, thyroid,
stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous,
cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
gene, ds.
                                                                                     4182 GGGCTCCTTGTGGGTGGGATCAGAACTAATCCAGAGTGGGGAAAGTGACAGTCAAAACCC 4241
153 CGGCAAGATGGCAGAGGTACGGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGA 94
                                                                                                                         93 GGGCTCCTTGTGGTGGGGATCAGAACTAATCCAGAGTGTGGGAAAGTGACAGTCAAAAGCCC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stomach cancer related gene sequence SEQ ID NO:2565.
                                                                                                                                                                                                     4242 CACCTGGAGCAAATAAAAAAACATACAAAACGT 4274
                                                                                                                                                                                                                                      33 CACCTGGAGCAAATAAAAAAACATACAAAAAGT 1
                                                                                                                                                                                                                                                                                                                                                                                                       ABL64228 standard; DNA; 273 BP
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18-SEP-2000

20-SEP-2000

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Control of the printed cancer disease states, disease progression, drug to monitor disease states, disease progression, but was obtained in electronic format directly from WIPO. The wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                              Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4062 GTGGGATTCATCCAGACTCATGCAATAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCT 4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4122 CGGCAAGATGGCAGAGGGTACGGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGA 4181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing and detecting the progression of liver cancer, the propercellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alvares C, Peres-Da-Silva S, Vockley JG;
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                                                                                                                                                                                                                                                                                                                                                                                Gene #3887 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3887; 298pp; English.
                                                                                                                                                                              ABN97389/c
ID ABN97389 standard; DNA; 273 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-2000; 2000US-237054P.
                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-426119/45.
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   3819 A 3819'
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical CC agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL501664 CC to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC activity and can be used in gene therapy. M1 can be used for screening CC an anti-neoplastic agent, and can be used for producing a product which cl is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC tructure and/or properties of the agent. M1 can be used in the CC treatment of cancer such as colon, breast, stomach, lung, thyroid, CC oesophageal, ovarian, kidney, prostate or pancreatic cancer, CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, CC cinfiltrating lobular cancer, squamous cell carcinoma, neuroendocrine CC carcinoma, papillary carcinoma and Wilm's tumour.
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Best Local S
Matches 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for anti-neoplastic agent involves exposing cells to chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature ger
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03-OCT-2000; 2000US-237608P.
01-NOV-2000; 2000US-244867P.
01-NOV-2000; 2000US-245084P.
              Human nervous system related polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 273 BP; 59 A; 74 C; 62 G; 78 T; 0 other;
                                                        23-JAN-2002
                                                                                                                                   ABA20255 standard; DNA; 546
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                                                                                                                                                                                                                                                                                                                                                                                         153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGGATTCATCCAGACTCATGCAATAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCT 4121
                                                                                                                                                                                                                                                        CACCTGGAGCAAATAAAAAAAAACATACAAAAACGT 4274
                                                                                                                                                                                                                                                                                                                                          GGGCTCCTTGTGGTGGGATCAGAACTAATCCAGAGTGTGGGGAAAGTGACAGTCAAAACCC 4241
                                                                                                                                                                                                                                                                                                                                                                                                             CGGCAAGATGGCAGAGGGTACCGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGA 4181
                                                                                                                                                                                                                                 CACCTGGAGCAAATAAAAAAAAACATACAAAACGT
                                                                                                                                                                                                                                                                                                          GGGCTCCTTGTGGTGGGATCAGAACTAATCCAGAGTGTGGGAAAGTGACAGTCAAAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273;
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Weaver 2
                                                        (first entry)
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                                                                                                                                   ВP
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 273;
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                  NO 12586
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30-JUN-2000;
07-JUL-2000;
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11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
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antiparasitic; cardiant; immune disorder; cardiovascular disorder;
neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, nootropic, neuroprotective, cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian, antisickling; antianaemic; antiarthritic; cancer; antiparkinematic; hepatotropic; cerebroprotective; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-2000;
02-MAR-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone amony. Preast, gastrointestinal tract, liver, lung, or unogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diaberes mellitus, Crohn's disease, multiple sclerosis, rhoundatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. crebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic infections.

Where The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences.
                                                                                                                                                                                                                                                                 Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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